APPLYING FOR INDEPENDENT RESEARCH BMB/MICRB 496

SdzƳƳŜNJĸCl-ff 2012

Application Deadline for **SUMMER/FALL 2012** is: **MARCH 2, 2012**

Faculty Interviews and Offers will be held week 09 - 11 of the semester**:** **MAR.12 – 30, 2012**

Arranging Independent Research (496) in the Department of Biochemistry & Molecular Biology

Due to the large number of undergraduate students and University Scholars, both within and outside the Department, who seek to participate in the ongoing research programs of BMB faculty, it has become necessary to establish guidelines for arranging Independent Research 496. Thus, the following policy will be in effect:

1. Students interested in participating in research should report to the department office in 107 Althouse to obtain a copy of the 496-Applicant Information Sheet. At that time, the student will be informed of 1) the faculty who have openings in their laboratories, 2) the research interests of BMB faculty so he/she can make informed choices, and 3) any qualifications individual faculty set for participation in 496 work (i.e., minimum GPA or semester standing). **Faculty will not consider a student for a 496 project without seeing a completed 496-Applicant Information Sheet.**

2. From the list of faculty members who have 496-positions available, the student will select four of the faculty with whom they would be most interested to work and indicate their selection on the back of the application form.

3. **APPLICANT INFORMATION SHEETS WILL BE DUE IN 107 ALTHOUSE BY THE END OF THE 8TH WEEK OF CLASSES FOR 496 POSITIONS TO BE FILLED THE FOLLOWING SEMESTER**. The deadline for admission to Summer session and Fall semester positions will be the eighth week of the preceding Spring semester.

4. Following receipt of the completed Applicant Information Sheet, the Department office will distribute copies of the Information Sheet and the student's transcript to the faculty listed by the student. If interested, a faculty member will contact the student to arrange an appointment to discuss the possibility of working in his/her laboratory.

5. If an appointment is arranged, the student should be prepared to discuss such topics as: 1) the number of credits to be scheduled, 2) the time commitment involved, and 3) his/her future goals.

5. During the 9th-11th weeks of the semester, faculty will hold interviews, make a decision, extend their offer(s) and request a response from the applicants. Faculty will notify the department office as their 496-positions are filled.

6. If a student does not hear from any faculty member within 3 weeks, the student may return to 108 Althouse and select another group of faculty who still have 496 openings at that time. This process may continue until all available faculty have been notified of the student's interest in securing a 496 position.

7. Students in majors other than BMB, Bioch, Micrb, or MCB must register for BMB or Micrb 496 to work with faculty in the BMB Department.

8. Upon acceptance by a BMB faculty member for a 496 project, the student must obtain the signature of the faculty member on a 496-Approval Form and return it to 108 Althouse to register for the course officially. It is not possible to preregister for 496 courses on eLion. The 496-Approval Form must be signed by the faculty member and returned to 108 Althouse each semester the student undertakes 496-Independent Research.

NOTE: BMB Students who arrange to do Independent Research with faculty who are not on the approved list will **NOT** be permitted to register for BMB or Micrb 496. For example, a student who arranges to do research with a faculty member in Food Science must schedule FD SC 496 NOT BMB 496. If it can be demonstrated that the work done in other departments is sound biochemistry, microbiology, or molecular/cell biology, the student may petition to count the course as BMB 496 to fulfill degree requirements. Petitions must be supported and signed by the student's professional adviser and approved by the Director of Undergraduate Programs. But, using the example above, the course will still appear as FD SC 496 on the academic transcript.

DEPARTMENT OF BIOCHEMISTRY AND MOLECULAR BIOLOGY
496-INDEPENDENT RESEARCH
APPLICANT INFORMATION SHEET

NAME	STUDENT NUMBER	MAJOR
LOCAL ADDRESS	**LOCAL PHONE**	**EMAIL**
SCHREYER SCHOLAR	**IF YES, NAME OF SCHOLAR ADVISOR**	**WHEN DO YOU WISH TO BEGIN YOUR 496 WORK?**
☐ YES ☐ NO		☐ SU ☐ FA ☐ SP
HOW MANY SEMESTERS ARE YOU WILLING TO COMMIT TO DOING RESEARCH?		

Faculty with whom you would be interested in working (CHECK FOUR):

BMB DEPARTMENT GRADUATE FACULTY

- ☐ Dr. Sarah Ades, 406 Althouse Lab
- ☐ Dr. Lucy Bai, 206 Life Science
- ☐ Dr. Marty Bollinger, 336 Chemistry
- ☐ Dr. Squire Booker, 302 Chemistry
- ☐ Dr. Jean Brenchley, 209 S. Frear Lab
- ☐ Dr. Donald Bryant, 106 S. Frear Lab
- ☐ Dr. J. Greg Ferry, 205 S. Frear Lab
- ☐ Dr. Richard Frisque, 103B Althouse Lab
- ☐ Dr. David Gilmour, 465 N. Frear Lab
- ☐ Dr. Ying Gu, 262 N. Frear Lab
- ☐ Dr. Wendy Hanna-Rose, 104D Life Scien.
- ☐ Dr. Ross Hardison, 304 Wartik Lab
- ☐ Dr. Eric Harvill, 124 Ag. Sc. Ind.
- ☐ Dr. Teh-hui Kao, 403 Althouse Lab
- ☐ Dr. Ken Keiler, 401 Althouse Lab
- ☐ Dr. Andrey Krasilnikov, 106 Althouse Lab
- ☐ Dr. Maria Krasilnikova, 206 Life Scien.
- ☐ Dr. Carsten Krebs, 322 Chemistry
- ☐ Dr. Zhi-chun Lai, 127 Life Science
- ☐ Dr.A. Lesk, 203 S. Frear Lab
- ☐ Dr.Bernhard Luscher, 221 Life Scien
- ☐ Dr. Andrea M. Mastro, 308B Althouse Lab
- ☐ Dr. Katsuhiko Murakami, 006 Althouse Lab
- ☐ Dr. Anton Nekrutenko, 505 Wartik Lab
- ☐ Dr. Gary Perdew, 309 Life Science
- ☐ Dr. Jeffrey Peters, 312 Life Scien.
- ☐ Dr. K. Postle, 301 Althouse Lab
- ☐ Dr. Frank Pugh, 458 N. Frear Lab
- ☐ Dr. Joseph Reese, 463 N. Frear Lab
- ☐ Dr. Melissa Rolls, 118 Life Science
- ☐ Dr. Lorraine Santy, 208 Althouse Lab
- ☐ Dr. Stephan Schuster, 310 Wartik Lab
- ☐ Dr. Song Tan, 468 N. Frear Lab
- ☐ Dr. Graham Thomas, 607A Mueller
- ☐ Dr. Ming Tien, 408 Althouse Lab
- ☐ Dr. Yanming Wang, 332 S. Frear

Applicant Name: ______________________________
Last Name, First

1. What are your career goals?

2. Briefly, explain your reasons for seeking a 496 research project.

3. What do you perceive to be your academic strengths/interests, if any?

4. What do you perceive as your academic weaknesses, if any?

5. How would you describe yourself to someone who never met you?

Please print completed application and return to 107L Althouse Lab.

Department of Biochemistry and Molecular Biology
Faculty Description
496 Independent Research – Open Positions

Faculty Name	Brief Description of Research Interests	Selection Criteria
Sarah Ades 406 Althouse sea10@psu.edu	The cell envelope of Gram-negative bacteria plays an essential role for the bacterial cell by providing a barrier between the cell and the environment, determining its morphology, and maintaining its structural integrity. The ability of the cell to respond to challenges to the cell envelope is of considerable medical importance as it is the target of several classes of antimicrobial drugs. The work in my laboratory focuses on identifying and characterizing the signal transduction pathways that communicate information between the cell envelope and the cytoplasm in Gram-negative bacteria. We use a wide variety of methods in our research including molecular biology, genetics, microarray analysis of gene expression, biochemistry, and microbial physiology	A strong interest in research and excitement about science. Must be willing to commit to 10 hours per week for at least 2 semesters. BMB, MICRB, BIOL majors preferred.
Lucy Bai 206 Life Science Building lub15@psu.edu	Bai lab is interested in studying the relation between chromatin and gene expression at single cell / single molecule level by using a combination of biophysical, biochemical, genetics, and computational methods. The long term goal of our lab is to identify sequence and chromatin features that affect the level, noise and dynamics of gene expression, to understand how these chromatin features are established and characterize their cell-to-cell variability and dynamic change, and finally, to explore how these molecular processes affect cell phenotype.	Candidates should have some basic knowledge / training in molecular biology and genetics, and are interested in quantitative biological problems.
J. M. Bollinger 336 Chem jmb21@psu.edu	I am interested in enzymes that use complex metal ion clusters to catalyze important and difficult chemical reactions (e.g. nitrogen fixation, water oxidation, alkane functionalization). In general, Nature has evolved far more elegant and effective strategies than chemists have yet devised to carry out these difficult reactions. In most cases, Nature's strategies depend on her ability to synthesize structurally diverse and complex clusters of metal ions for use as catalytic cofactors. Thus, a primary objective of our research is to understand the mechanisms by which Nature assembles these clusters into the proteins in which they ultimately function as catalytic centers.	Strong background and interest in chemistry and physics
Squire Booker 302 Chem sjb14@psu.edu	Our laboratory is endeavoring to understand at the detailed molecular level the reaction mechanisms employed by select enzymes that use cofactors or co-substrates in catalysis. One major research focus is to understand enzymatic reactions in which S-adenosyl-*L*-methionine is employed. S-adenosyl-*L*-methionine, which is called SAM-e by non-scientists, and AdoMet by scientists who study it, has been implicated in a broad range of diseases, including among many others, cancer, arthritis, fibromyalgia, and depression. It is approved in many European countries as therapy for several of these diseases, but is sold over-the-counter in the United States as a supplement. In order to address the specific role of AdoMet in any type of malady, a firm understanding of its chemical reactivity in general must be appreciated. Unlike most cofactors or co-substrates in biochemistry, which are typically dedicated to one particular type of reaction, AdoMet has been shown to be involved in two types of group transfer reactions, which likely proceed by drastically different reaction mechanisms, as well as the initiation of radical-dependent enzymatic transformations. Our goal is to characterize these various reaction pathways in detail, and use information gained to locate possible targets for pharmaceutical development.	Must have a strong background in chemistry, biochemistry, or molecular biology, and be excited about science.

Faculty Name	Brief Description of Research Interests	Selection Criteria
Jean E. Brenchley 209 S. Frear jeb7@psu.edu	Our research objective is to discover and characterize novel microorganisms and their useful cold-active enzymes. This involves isolating cold-loving, psychrophilic microorganisms and screening ones making enzymes with high activity at low temperatures. Enzymes of interest include β-galactosidase, alkaline phosphatase and proteases that have potential industrial uses. Enzymes having the desired properties are characterized biochemically and genetically. Our work not only adds to the fundamental understanding of protein structure, but can lead to enzymes important for processing refrigerated foods, for treating wastes in cold climates, and for catalyzing low-temperature industrial reactions. We are also studying the microbial diversity in permanently frozen environments (the Greenland ice sheet, Antarctic Vostok ice). We examine the abundance and viability of microbial populations in these harsh habitats and develop procedures for their recovery. Another goal of our research is linking microbial diversity with biogeochemical activity within ice cores. Students working in the lab can gain experience involving microbiology, biochemistry, microbial phylogenetics, and molecular biology depending on their interest and the project they select.	Must be enthusiastic, motivated, self-disciplined, and hard-working. Several semester commitment required.
Donald Bryant 106 South Frear dab14@psu.edu	My laboratory uses genome-sequence-enabled, molecular genetics and recombinant DNA methods to study two fundamentally different types of photosynthetic bacteria: the marine, oxygen-evolving cyanobacterium *Synechococcus* sp. PCC 7002 and the strictly anaerobic green sulfur bacterium *Chlorobium tepidum*. Both organisms are naturally transformable and thus amenable to genetic manipulation. The complete genomic sequence (2,154,946 bp) of *C. tepidum* has been determined in collaboration with The Institute for Genomic Research, and we have determined the sequences for 11 other green sulfur bacteria. The 3.4 Mbp genomic sequence of *Synechococcus* sp. PCC 7002 has also been determined in collaboration with Dr. Jindong Zhao (Peking University and the Institute of Genetics, Beijing, PRC) and Stephan Schuster. The availability of the genomic sequences for these organisms greatly facilitates the identification of genes of interest for more detailed studies. The laboratory is presently studying several different aspects of these organisms. These include structural and functional relationships of the Photosystem I reaction center and other electron transport complexes and proteins; structure, function and assembly of light-harvesting complexes in both organisms; carotenoid and chlorophyll biosynthesis in both types of organisms; the biogenesis of Fe/S clusters cyanobacteria; and biosolar hydrogen production and the development of chlorophototrophs as agents for biofuels production. A new project in the lab is the biochemical and physiological characterization a completely new phototrophic microorganism isolate from hot spring microbial mats in Yellowstone National Park. Projects for undergraduates provide hands-on experience with modern molecular biological methods as well as biochemical methods and microbial physiology.	Minimum GPA > 3.00 Majors: BMB or MICRB; Prefer Honors students and a commitment of at least 3 semesters.
J. Greg Ferry 205 S. Frear jgf3@psu.edu	All life is classified into one of three "domains." Procaryotes in the Archaea domain evolved separately from eubacteria (Bacteria domain) and are more closely related to eucaryotes (Eucarya domain). We study the enzymology and molecular biology of anaerobic microbes from the Archaea domain with the goal to discover new principals and applications of fundamental cellular processes common to all three domains. For example, two enzymes under investigation (acetate kinase and phosphotransacetylase) are key to obtaining energy for several pathogenic anaerobes. Studies on the mechanisms of these enzymes are designed to identify inhibitors with the potential to become new classes of antibiotics. Our studies have also led to the discovery of several enzymes with novel structures and functions. These include a new family of iron-sulfur flavoproteins and a new class of carbonic anhydrase present in all three domains of life. Our research on ancient enzymes from the Archaea is contributing to an understanding of the origin and evolution of life and directly impacts the emerging field of Astrobiology. Graduate students and postdoctoral associates interact with the Penn State Astrobiology Research Center. Functional genomics plays a central role in the research. We have obtained the sequence of the entire genome of	Prefer junior year students with at least a 3.00 GPA and willingness to work through the summer between their junior and senior years.

Faculty Name	Brief Description of Research Interests	Selection Criteria
	Methanosarcina thermophila (a methane-producing anaerobe from the Archaea domain) in collaboration with private industry. Microarray (DNA chip) analysis of the genome is leading to the discovery of still more novel enzymes for which investigations into structure/function await.	
Richard J. Frisque 103B Althouse rjf6@psu.edu	Pathogenic and oncogenic potential of the human virus; JC virus; Genetic, molecular and biochemical approaches. Our laboratory's research interests center on the unique biology of the human polyomavirus, JC virus (JCV). In the following regards, JCV differs from the other members of the Polyomavirus genus: 1) JCV is the causative agent of a fatal disease (progressive multifocal leukoencephalopathy [PML]) in its natural host; 2) it transforms cells in culture very inefficiently, but induces a wide variety of tumors in hamsters; it is the only human virus known to cause solid tumors in primates; 3) JCV demonstrates an exceedingly narrow host range in vitro, and during passage in culture tends to undergo genomic alterations, 4) JCV expresses 5 tumor proteins from alternatively spliced transcripts.	Minimum 3.0 GPA Enthusiasm for research required Commitment to 3 or more semesters
David Gilmour 465 N. Frear dsg11@psu.edu	We study transcriptional regulation of the hsp70 gene in Drosophila. This gene has emerged as a paradigm for understanding transcriptional control at the level of elongation. Elongation is the stage of transcription when nascent transcript is being polymerized. Other genes exhibiting this type of control include the proto-oncogenes c-myc and c-fos. Transcription of HIV is also controlled at the level of elongation. We are using biochemical, genetic, and molecular genetic approaches to understand transcriptional regulation of hsp70. For more information, see: http://bmb.psu.edu/directory/dsg11	Minimum commitment of 3 semesters. B or better in BMB/Micro 251 or an equivalent course.
Ying Gu 262 N. Frear yug13@psu.edu	Cellulose, composed of β-1, 4 linked glucan chains, is the most abundant biopolymer on earth. Cellulosic biomass is an abundant renewable resource that has been recently targeted for the production of alternative transportation fuels. However, little is known how cellulose is produced and how the biopolymer is assembled. My main objective is to characterize the molecular and cellular mechanisms controlling cellulose biosynthesis in higher plants. My lab uses live cell imaging to visualize the cellulose synthesis machinery in living plant cells. Through molecular, biochemical, and genetics approaches, we identified several proteins that could potentially involve in the assembly, delivery, and regulation of the cellulose synthesis machinery. We aim to unravel the mystery of cellulose biosynthesis as technology, genetic and genomic tools are well developed, particularly in *Arabidopsis*. Considering cellulosic biomass are expected to become one of the main sources of biomass for the production of renewable biofuels in the near future, the data generated through our research may be of great interest for energy producing agents.	Highly motivated, hard-working individual who is willing to commit 15 hours per week for at least 2 semesters. Background in molecular biology preferred. Minimum GPA-3.0. No seniors.
Wendy Hanna-Rose 104D Life Science wxh21@psu.edu	Our goal is to understand the genes and the molecules that direct the development of organs. By understanding how organs are formed, we hope to shed light on the mechanisms that sometimes malfunction during development, resulting in certain birth defects. To approach this problem, we focus on understanding the developmental programs of the uterus and the vulva in the model organism C. elegans. The C. elegans vulva is a tube formed from only 22 cells that connects the uterus to the outside of the body. We have identified several genes that act to promote a proper connection between the vulva and the uterus. In our research, we use a variety of genetic and molecular approaches to decipher the molecular functions of these genes. Please refer to website for more specific details: http://bmb.psu.edu/directory/wxh21	Enthusiastic, highly motivated, hard-working student; commitment of 10 hours per week for several semesters, sophomore preferred, freshman under exceptional circumstances; no seniors

Faculty Name	Brief Description of Research Interests	Selection Criteria
Ross C. Hardison 304 Wartik rch8@psu.edu	**Functional genomics of noncoding DNA: Regulation of mammalian hemoglobin genes** The determination of almost complete genomic DNA sequences from many species, including humans, is revolutionizing biological sciences. While the first wave of post-genomic analysis is focused on identifying the protein-coding portions of the genome, that effort will account for only about 3% of the genomic DNA in mammals (and other species). Another 40-45% of the human genome is repetitive DNA generated by retrotransposition. That leaves about half the genome (noncoding, nonrepetitive DNA) to analyze. Although some parts of this DNA within introns or between genes may have no discernable function, other regions are involved in regulating the expression of the genes. Regulation of expression is important to understand both for fundamental issues in developmental biology and for exploring novel avenues to explore for therapeutic advances, improvement in agriculture, etc. Hence it is critical to find the regions of noncoding, nonrepetitive DNA that are likely to be involved in an important function, such as gene regulation. A long-standing collaboration with Dr. Webb Miller (Computer Science and Engineering) has generated computer tools to aid in finding strong candidates for functional sequences in noncoding DNA, culminating in our PipMaker and MultiPipMaker servers, which can align two or more genomic DNA sequences of any length and display the results in a compact, easily understood display (a percent identity plot). In an further collaboration with the Mouse Sequencing Consortium and labs at Univ. California Santa Cruz, we have now computed such plots for the entire available human and mouse genomes and provided them on the Internet. Other resources specific for mammalian globin gene analysis were developed and are available at the Globin Gene Server. These include tools for analyzing a multiple alignment of beta-globin gene clusters, databases of hemoglobin variants and thalassemias, and a database of experimental results on globin gene regulation. One of the strengths of this program has been the combination of experimental tests along with the development of new software. Our work over the past decade has demonstrated repeatedly that previously unstudied, but conserved, sequences within the beta- and alpha-globin gene clusters are involved in regulation. Hence the validity of this approach is well documented. One current challenge is to analyze the patterns of conservation across the entire human genome to develop a deeper picture of mammalian genome evolution and to provide better candidates for regulatory elements. We continue to work on methods for testing these candidate regulatory regions as well as proteins implicated in acting at them. Web sites: PSU Bioinformatics and servers http://bio.cse.psu.edu Globin Gene Server http://globin.cse.psu.edu Hardison Lab web site http://bmb.psu.edu/directory/rch8	Grade point average at least 3.0 Honors students preferred Commitment of at least 3 semesters highly preferred

Faculty Name	Brief Description of Research Interests	Selection Criteria
Eric Harvill 124 Ag. Sci. Ind. harvill@psu.edu	Bacteria that cause persistent infection have, in some cases, evolved mechanisms that allow them to manipulate host immune responses to avoid clearance. We are examining these mechanisms using a bacterium that is naturally highly infectious in mice and other animals, causes a range of respiratory diseases and persists for the life of the animal despite an active immune response, characteristics indicative of a highly evolved bacterium-host interaction. Bordetella bronchiseptica subspecies pertussis infects humans and is the etiologic agent of whooping cough, which is amongst the most important bacterial respiratory diseases in the world, killing hundreds of thousands of children yearly. Bordetella bronchiseptica is very closely related to Bordetella pertussis, but displays a very broad host range, causing kennel cough in dogs, atrophic rhinitis in pigs and snuffles in rabbits. Bordetellae can be manipulated genetically, allowing the role of individual virulence factors to be probed at the molecular level. Since B. bronchiseptica naturally infects mice, all the tools of mouse molecular immunology can be used to probe the host factors important in the interaction. We have combined the tools of bacterial genetics and mouse molecular immunology to better understand bacterial virulence factors, host immune functions, and the complex interactions involved in persistent bacterial infections. http://www.vetsci.psu.edu/personnel/faculty/harvill.cfm	10+ hours per week for four+ semesters and/or summers.
Teh-hui Kao 403 Althouse txk3@psu.edu	The lab is interested in cell-cell communication and signal transduction during pollen development and pollination in flowering plants. One major area of focus is a self/non-self recognition mechanism called self-incompatibility, which allows the female reproductive organ, the pistil, to distinguish between self and non-self pollen. Self pollen is rejected whereas non-self pollen is accepted for fertilization. Thus, self-incompatibility prevents inbreeding and promotes outcrosses, and is beneficial to plants. Our ultimate goal is to use molecular genetic and functional genomic approaches to identify all the genes involved in the recognition and rejection of self pollen, and decipher the biochemical mechanism of this process. Another focused area of research is a receptor-kinase mediated signaling pathway that we have shown to be required for the progression of microspores (immature pollen grains) from the unicellular stage to the bicellular stage. We are interested in identifying all the proteins that directly or indirectly interact with this kinase and determining how all the components of this pathway function to regulate pollen development. *Petunia inflata*, a wild relative of garden petunia, is used for all the studies.	Minimum GPA - 3.00 3-4 credits each
Kenneth Keiler 401 Althouse kkeiler@psu.edu	We are interested in how bacteria regulate when and where proteins are expressed. In order for bacteria to control cell cycle and developmental programs, they must be able to express the appropriate proteins at the specific time and in the specific place where they are needed. We are investigating a mechanism of translational control mediated by a very unusual small RNA, called tmRNA or SsrA RNA. tmRNA is a highly abundant RNA found in all bacteria. It alters the expression of substrate proteins by intervening during translation of the mRNA to target the nascent polypeptide for proteolysis, and to release the translating ribosomes from the mRNA. We have found that tmRNA is required for regulation of the cell cycle and development in *Caulobacter crescentus*, and we are using biochemical and genetic approaches to understand the molecular events which underlie the tmRNA mechanism and to understand the role of tmRNA in bacterial differentiation and physiology. We are also using bacterial genetics and epifluorescence microscopy to identify localized proteins and to dissect the localization signals within these proteins.	Strong interest in research willing to commit to 5-10 hours per week for at least 2 semesters

Faculty Name	Brief Description of Research Interests	Selection Criteria
Andrey Krasilnikov 106 Althouse ask11@psu.edu	We are interested in learning the atomic-resolution details of the spatial organization of highly structured RNA molecules and complexes of such molecules with RNA-binding proteins. Using X-ray crystallography we can determine the three-dimensional structure of the molecule to the finest details; using a combination of crystallographic and biochemical studies we can answer a very broad variety of fundamental questions, ranging from the mechanisms of substrate recognition and catalysis to the structural and functional roles of individual parts of the molecule or complex.	High motivation; commitment to spend at least 10 hours per week for at least 3 semesters; a decent science GPA.
Maria Krasilnikova 206 Life Science Bldg. muk19@psu.edu	We study inherited diseases caused by expansion of trinucleotide repeats (repeated stretches of GGC, GAA, CAG) at specific positions in the genome. Those expansions cause severe neurological disorders, which worsen with age and finally lead to disability and premature death. The mechanisms of trinucleotide diseases still remain a mystery and there is currently no cure. To understand the mechanisms of those diseases we monitor how transcription and replication are going through those repeats in the model systems, including mammalian cultured cells. We use cloning, two-dimensional electrophoresis, southern and northern hybridization.	Highly motivated students. Minimum GPA 3.0. Willing to spend in the lab 5-10 hours a week.
Carsten Krebs 322 Chem ckrebs@psu.edu	The importance of iron as an essential element is underscored by the fact that iron-containing proteins play a pivotal role in almost every aspect of life. Our laboratory uses spectroscopic techniques, such as Mössbauer, EPR, and UV/VIS, to obtain detailed information about the nature of the Fe-sites in these proteins. When these spectroscopic methods are combined with kinetic techniques (rapid freeze-quench, stopped flow), it is possible to monitor the changes of the iron during a reaction and consequently, these studies allow us to determine the reaction mechanism of such enzymes.	Strong background and interest in chemistry and physics required. Must be sufficiently motivated to work 10 or more hours for 3 or more semesters. Honors program preferred.
Zhi-Chun Lai 127 Life Science Building zcl1@psu.edu	Our research focuses on 1) molecular genetic studies of regulatory genes that control neural morphogenesis and cell fate in the development of *Drosophila* visual system; 2) investigation of the role of Hippo tumor suppression pathway in coordinating cell proliferation and programmed cell death during development and tumorigenesis.	Strong interest in developmental genetics and cancer biology; sophomore or junior; 3 credits/semester for 3 or more semesters.
Arthur Lesk 203 South Frear aml25@psu.edu	To understand the mechanisms and pathways of protein evolution, we take advantage of the large amount of amino-acid sequence and protein-structural information available in databases. Projects appropriate for students would include analyzing sequence-structure relationships in families of proteins. The work would involve learning how to run standard bioinformatics software, and writing simple programs.	A curiosity about protein-structure, and facility with using computers, including some programming skills.
Bernhard Luscher 221 Life Science bxl25@psu.edu	We are using molecular biology, biochemical and genetic tools to address the structure, function and development of inhibitory synapses in the central nervous system (CNS). Neural inhibition in the brain is mediated mostly by the neurotransmitter gamma-aminobutyric acid (GABA), acting at postsynaptic GABA-A receptors. These receptors are targets of a large variety of therapeutically important drugs (the benzodiazepines) that include anxiolytics, tranquilizers, hypnotics, amnesics, muscle relaxants, and anti-epileptics. GABA-A receptors are therefore critically involved in the modulation of corresponding brain states. On the surface of neurons, most GABA-A receptors are concentrated at postsynaptic sites, apposed to GABA-releasing axon terminals. We are studying the molecular mechanisms and proteins that lead to clustering of GABA receptors at these membrane specializations. This mechanism modulates the efficacy of GABA transmission and thereby controls the CNS states listed above including learning and memory. As part of a second line of research we have generated GABA-A receptor deficient mice as an animal model of anxious depression. These mice show molecular, cellular, pharmacological, behavioral, and cognitive aspects of this disorder. We are using these mice to further elucidate the mechanism that leads to major depressive disorder. http://homes.bio.psu.edu/people/Faculty/Luscher/homepage.htm	Sophomores with GPA > 3.3 preferred. Outstanding freshmen accepted under certain conditions; student should be interested in preparing for graduate school in neuro-science; minimally 15 hrs/week, ≥ 4 semesters.

Faculty Name	Brief Description of Research Interests	Selection Criteria
Andrea Mastro 308B Althouse a36@psu.edu	My laboratory is interested in breast cancer metastasis to bone. In particular we wish to determine what happens to bone cells when they are in contact with the metastatic cancer cells. We hypothesize that the osteoblasts, normally bone rebuilding cells, are affected by the cancer cells so that they are no longer able to rebuild bone. Thus the bone resorption by osteoclasts goes unchecked. We are also examining the possibility that cancer cells cause osteoblasts to undergo apoptosis. Recently we have been using a bioreactor culture device to grow bone for long times. When cancer cells are added to the "bone tissue" they show many of the characteristics seen in vivo.	Minimum GPA – 3.20 Lab courses; Majors: BIOL, MICRB, BMB, MCB, BIOCH Honors Scholars, Howard Hughes, Wise; Freshmen accepted under certain conditions; sophomores and juniors ideal; seniors too late. At least 10 hrs/week; 2-3 semesters MUST BE COMMITTED
Katsuhiko Murakami. 006 Althouse kum14@psu.edu	Transcription is the major control point of gene regulation and RNA polymerase (RNAP) is the central enzyme of transcription. The long-term goal of this laboratory is to understand the mechanism of transcription and its regulation. We are particularly interested in determining X-ray crystallographic structures of RNAPs from different kind of organisms, e.g., bacteriophage (single-subunit RNAP), bacteria and archaea (multi-subunit cellular RNAP), and influenza virus (RNA-dependent RNAP). Based on the structures, we study the detailed functions of RNAP using biochemical and biophysical methods.	A strong interest in research and excitement about science. Must be willing to commit to 10 hours per week for at least 2 semesters. BMB, MICRB majors preferred
Anton Nekrutenko 505 Wartik Lab anton@bx.psu.edu	My laboratory will be working on a variety of problems that can be formulated and solved within the framework of comparative genomics. Below I list some of the projects. These projects represent only a small sample of fascinating questions that can be answered by comparing genomic sequences. Comparative approach to gene annotation. Application of comparative genomics to gene prediction is an intuitive and simple way to increase its accuracy and reliability. My lab will be pursuing the following directions: * Establish an alternative estimate of protein-coding capacity of the human genome using a comparative approach to challenge the current estimate of gene number in the human genome; * Develop a comparative approach for the assembly of the entire gene structure including identification of exon/intron boundaries and untranslated regions. Annotation of promoters. It appears that the gene number does not reflect the complexity of a given organism: humans only have between 30,000 and 40,000 genes, which is only a two-fold increase over C. elegans. Thus we think that the study of regulatory regions will provide answers to many fundamental evolutionary and genetic questions. Almost all currently used promoter-prediction algorithms suffer from the problem of overprediction (very high rate of false-positives). We are going to initially approach this problem by identifying groups of conserved regions and studying their combinations. Development of innovative web-based tools and databases. See http://nekrut.bx.psu.edu Evo-bio project. With new genomes coming out of sequencing centers every week, comparative analysis becomes the most powerful approach to unraveling the biological meaning of genomic sequences. Comparative genomics relies heavily on algorithms developed by evolutionary biologists. However there is a problem — implementation. The idea of evo-bio project is to develop a set of PERL-modules implementing numerous sequence analysis algorithms developed by evolutionary biologists.	GPA 3.0 or above Willingness to learn computational techniques in biology. Willingness to commit to 5-10 hours per week for at least 2 semesters

Faculty Name	Brief Description of Research Interests	Selection Criteria
Gary Perdew 309 Life Science ghp2@psu.edu	We are interested in determining the molecular mechanisms of toxicity of dioxin (TCDD) and other polycyclic aromatic hydrocarbons (e.g. benzo(a)pyrene). In addition, we are determining how the Ah receptor, which mediates the biological activity of dioxin, is regulated. The role of the Ah receptor in normal biological processes is also being examined. In particular we are purifying endogenous compounds that activate the Ah receptor. Another area of interest is in the role of heat shock proteins in regulating the activity of the peroxisome proliferator-activated receptor (PPAR). We use a wide variety of techniques including; protein biochemistry, molecular biology, transgenic mice, cell culture, microarrays, etc.. All techniques are used in the context of mammalian cell culture models.	Strong interest in experimental science. Minimum commitment of 2 semesters and 10 hours per week. GPA= 3.0, sophomores, juniors or seniors. Willing to work through the summer a plus.
Jeffrey Peters 312 Life Science jmp21@psu.edu	Our laboratory is interested in delineating biological sites of peroxisome proliferator-activated receptors (PPARs) in lipid homeostasis and cancer; the molecular regulation mediated by PPARs; and modulation of atherosclerosis and cancers through dietary or chemical activation of PPARs. Null mouse models are used extensively for these purposes. For more information about our laboratory, refer to the following website: http://www.cas.psu.edu/docs/CASDEPT/VET/JPeters.htm	Minimom GPA 3.00, 10+ hours per week for 4+ semesters.
Kotty Postle 301 Althouse kup14@psu.edu	Pathogenic gram-negative bacteria use the TonB system to steal iron from hosts. The TonB system is also a way that iron, an essential nutrient, gets into the food chain (without which, of course, we would all die). We study the mechanism of TonB-dependent iron acquisition using E. coli as the model system. It involves an interesting series of signal transduction events at both cytoplasmic and outer membranes. We use biochemistry, genetics, and molecular biology to find out how it works with the aim of developing novel antibiotics that target iron uptake. http://bmb.psu.edu/directory/kup14	Strong interest in experimental science; must have taken some science laboratory classes with Micro 202 preferred. Minimum science GPA of 3.2. Expect to work at least 10 hr/wk for at least 2 semesters.
Frank Pugh 458 N. Frear bfp2@psu.edu	One important difference between a normal and cancerous cell is how they regulate the expression of their genes. A critical aspect of regulation is shifting protein-protein and protein-DNA interactions at the control or promoter region of a gene. Proteins assemble into transcription complexes at promoters, which regulate how often individual genes are transcribed into RNA copies of those genes. Different cells have different amounts and varieties of RNAs, which are translated into different amounts and varieties of proteins, the primary building blocks of cells. The protein constituents of cancerous cells are out of proportion to what is found in healthy cells. Dr. Pugh's research is directed toward defining the shifting interactions that lead to the assembly and regulation of transcription complexes. One central component of transcription complexes is the TATA binding protein or TBP, which binds to gene promoters and coalesces the assembly of transcription complexes. Many gene activators work by recruiting TBP to promoters, and many repressor act to block TBP. Students use the tools of biochemistry, molecular biology, genetics, and genomics to investigate the functional interplay of these activator and repressors, with an eye toward understanding fundamental mechanisms of gene regulation. Knowledge of the molecular events governing gene expression will lead to insights into how changes in gene expression turn healthy cells cancerous. More information can be obtained at http://bmb.psu.edu/directory/bfp2	Minimum GPA - 3.0 Honors students Freshman or Sophomore

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Joseph Reese 463 N. Frear jcr8@psu.edu	Eukaryotes activate two known resistance pathways in response to ultraviolet (UV) radiation. The first is the well-known DNA damage sensing, signaling and repair pathway that is stimulated exclusively by damage to DNA. Activation of this pathway causes the execution of cell cycle delays, referred to as checkpoints, and the expression of DNA repair genes. The second less characterized, but nonetheless equally important, pathway is mediated by the proto-oncogene RAS, mitogen activated protein kinases (MAP) and a class of transcription factors commonly referred to as AP-1 like transcription factors. This pathway is thought to respond to the non-genomic effects of UV irradiation, such as organelle damage. Alterations in either of these two pathways are known to predispose people to cancer and other diseases. Our laboratory uses a combination of biochemistry, genetics and molecular biology to study the regulation of these two resistance pathways in the simple eukaryote *Saccharomyces cerevisiae*. URL: http://bmb.psu.edu/directory/jcr8	3.2 Science GPA BMB, MCRB or Biology majors Interest in a career in biomedical research Highly motivated Freshman (Honors College) and sophomores. No seniors 8-15hrs per week with at least two >3hr blocks of time
Melissa Rolls 118 Life Science mur22@psu.edu	We are interested in the subcellular organization of neurons. Neurons are specialized to integrate information and to send signals over long distances. A fundamental part of this specialization is the division into axons, dendrites and cell body. We study how these three major compartments are established and maintained using Drosophila genetics and confocal microscopy. One of the major projects is to understand how the microtubule cytoskeleton differs between axons and dendrites, and how these differences contribute to polarized trafficking of proteins in neurons. We are also studying neuronal responses to injury including regeneration.	Undergraduates who join the lab must be highly motivated, spend at least 10 hours/ week in the lab, for 2 or more semesters, and be able to stay in the lab for 1 or more summers.
Lorraine Santy 208 Althouse Lab lcs13@psu.edu	The ability of cells to move about is an important component of tissue development and injury repair. Cellular migration requires precise spatial and temporal coordination of alterations in cellular signaling and architecture. Numerous members of the Ras Superfamily of small GTPases regulate aspects of this behavior. We are studying the role of one of these GTPase families, the ADP-ribosylation factors or ARFs, in regulating motility of epithelial cells. Projects in the lab focus on the regulation and sub-cellular localization of ARF activity, and on the signal transduction cascades regulated by the ARFs. Techniques in use include mammalian cell culture, molecular biology and biochemistry.	Enthusiastic, disciplined and self-motivated students who are interested in learning about scientific research. With a minimum GPA 3.0. Willing to commit 5-10 hours/wk for at least 2 semesters.
Stephan Schuster 310 Wartik Lab scs19@psu.edu	http://bmb.psu.edu/directory/scs19	
Song Tan 468 N. Frear sxt30@psu.edu	Our laboratory is interested in how genes are turned off or on since such regulation is altered in cancer cells. Our goal is to determine how gene regulation complexes work using both biochemical and structural approaches. A focus of the lab is to determine the three-dimensional structure of chromatin complexes by X-ray crystallography. Current undergraduate projects include (a) coexpression of protein complexes in *E. coli*, (b) affinity purification of proteins, and (c) characterizing chromatin enzymes through pulldown and enzyme assays. For more information, please visit our web site at: http://www.personal.psu.edu/sxt30/positions_undergrad.html	Highly motivated freshmen, sophomores or juniors in honors program preferred.

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Graham Thomas 607A Mueller gxt5@psu.edu	We are interested in the role of the actin cytoskeleton in epithelial morphogenesis – how do the cells in such tissues perform cell shape changes in such a way as to generate specific forms we see in fully developed tissues and organs? Current research focuses on the membrane associated protein spectrin and uses the fruit fly *Drosophila melanogaster* as a model system for these investigations because of the wide range of genetic, molecular and cell biological tools that this makes available to us. The specific projects available to undergraduates are always in flux, but recent examples include traditional and transgenic genetic experiments, immunofluroescent localization of protein purification, antibody epitope mapping. We are also interested in the evolution of spectrin and have projects available in this area too. The exact techniques used will depend on the specific project picked. These could include molecular biology (Polymerase chain reaction, DNA gels and Southern blots, protein gels and Western blots, plasmid cloning and protein expression, restriction analysis etc.), cell biology (immunofluorescent analysis of protein distributions, time lapse imaging of live cells and embryos labeled with Green Fluorescent Protein (GFP), digital microscopy, etc.), genomic database searching and sequence analysis, and genetics (both classical and transgenic). http://bmb.psu.edu/directory/gxt5	Minimum Science GPA 3.3 Majors: Biol, BMB, Micrb Expectations/Requirements: 2-3 credits (4.5-5 hours per credit/week), preferably sophomores or juniors with interest in long-term relationship with lab (i.e., spending several semesters in lab, interest in doing summer research); however, willing to consider freshmen and seniors if sufficiently enthused by our work. Honors thesis projects available. Biol 230W or BMB/MICRB 251/252 an advantage.
Ming Tien 408 Althouse Lab mxt3@psu.edu	The Tien lab's current research centers on the study cellulose synthesis employing classical biochemical approaches. We use three model organisms, *Arabidopsis thaliana, Physcomitrella patens,* and *Gluconacetobacter hansenii*, in order to interrogate the proteins responsible for cellulose synthesis. In plants, the cellulose synthase catalytic subunits (CesAs) form a large complex in the plasma membrane, from which they extrude cellulose into the cell wall. However, very little is known about how these proteins function, in fact, a complete understanding of the complex composition is still unknown. Our research goals are aimed at uncovering some of this unknown information so we can fundamentally understand how these complexes, and their member proteins, function. We hope that the fundamentals we discover can pave the way for future scientists to improve upon and modify the complex and the CesA proteins in order to produce cellulose that can be better utilized for production of biofuel and material science. Research in Tien lab is geared towards the biochemical characterization of proteins. Undergraduate researches will gain experience with a vaiety of classical biochemical techniques including SDS-PAGE, western blotting, column chromatography, protein expression and purification, enzyme kinetics, chemistry, proteomics, and crystallography, as well as various molecular genetics techniques.	A commitment of 10-15+ hours per week for at least 2 semesters required. GPA at least 3.0. BMB majors preferred, though others will be considered. Likewise, juniors preferred, but we will also consider sophomores and seniors (if you have at least 2 semesters of coursework remaining).
David Tu 203A N. Frear unh@psu.edu	Gene expression, protein structure and function. Students will work with the professor in person. A typical project right now will be to analyze the transposon insertion site sequences for several transgenic fly lines that show interesting phenotypes.	Minimum GPA - 3.30 (unless science GPA is 3.50 or better). Prefer Honors students doing thesis.
Yanming Wang 454 N. Frear yuw12@psu.edu	My laboratory studies a histone deiminase, termed PAD4/PADI4, which converts both Arg and methyl-Arg residues in histones to citrulline. We found that histone citrullination is important for trapping and killing bacteria by neutrophils extracellular traps, a chromatin based web-like structure. In addition, PAD4 interacts with the tumor suppressor p53 to repress the expression of tumor suppressor genes thereby facilitating tumorigenesis. Our ongoing research with PAD4 inhibitors is highly promising to offer new treatment of cancer and autoimmune disorders.	

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	http://bmb.psu.edu/directory/yuw12	