Abstract Guidelines

Please submit an approximately 250 word abstract summary. This statement will appear in print in the SOURCE Symposium and Poster Summary Guide on the web. This statement is central to your proposal and must provide a succinct overview of your larger work (i.e. poster, paper, performance).

Please incorporate the following guidelines before submitting your abstract statement.

- Times New Roman, 10 point font
- At the top of the page, bold and center the proposal title
- Bold all undergraduate students' names who will serve as presenters for this project. Provide academic majors of the student presenters.
- Provide the names and department affiliation of all others who contributed to the project (e.g. Graduate Students, Post Doctoral, Lab Staff Members, etc.)
- Double space and provide the abstract summary. Single space within the paragraph.
- Double space and italicize your faculty mentor's name and provide the department affiliation.
- The document should be submitted as a Word document. A pdf is not acceptable.

If you have questions, please do not hesitate to contact Sheila Pedigo (sheila.pedigo@case.edu) or Bethany Pope (bethany.pope@case.edu) in the SOURCE office.

<u>Sample Abstracts</u>

Modeling the Vasopressin V2-Renal Receptor and Predicting Interaction with Non-Peptide Antagonists

Nicholas Callahan, Department of Biochemistry; Rosemarie M Dazard, Department of Biochemistry; and Menachem Shoham, Department of Biochemistry

Vasopressin is a peptide hormone implicated in kidney, heart and brain function. The Vasopressin-2 receptor is a seven-helix transmembrane G-protein coupled receptor, which plays in a role in water reabsorption and vasodilatation. This research is concerned with creating a computer model of the Vasopressin-2-renal receptor, then using this model to predict how vasopressin and non-peptide antagonists dock to the receptor. We have also investigated how mutations in the receptor would alter the affinity of the antagonists to the receptor. Experiments are underway to experimentally measure the affinity of the compounds to wild type and mutant receptors. The antagonists are OPC21268, OPC31260, OPC41061 obtained from Otsuka Pharmaceuticals (Japan) and SR49059, SR121463B, and SSR149415 obtained from Sanofi Pharmaceuticals (France).

Project Mentor: Professor Menachem Shoham, Department of Biochemistry

A Multiplex PCR-LDR Assay for Polymorphism Determination in Plasmodium falciparum pfmdr1 Gene

Eric Carnevale, Department of Biology; Dr. Peter Zimmerman, Global Health and Disease

Resistance to antimalarial drugs such as chloroquine (CQ) has significantly increased the mortality rate of malaria infections in the past several decades. Because of this a greater understanding of the mechanisms behind CQ resistance is required, and specifically the role played by the *Plasmodium falciparum* gene pfmdr1. Single nucleotide polymorphisms (SNPs) have been identified in this gene, that are thought to contribute towards the parasite's ability to withstand treatment. Because of this we are developing an assay that can identify supposed resistance genotypes quickly, reliably, and with the capacity for processing many samples at once. A standard PCR amplifies target DNA, which is then followed by a ligase detection reaction (LDR). The LDR interrogates the SNP by binding an upstream probe that is allele specific and tagged with a 5' sequence to hybridize to a polystyrene bead, and a downstream probe that anneals to a conserved sequence and is bound to biotin on the 3' end to hybridize to a fluorescent molecule. Detection involves hybridizing the LDR product to fluorescent r-phycoerythrin for quantification, and to a unique, fluorescent, polystyrene bead for allele identification. The process has been shown to accurately identify the pfmdr1 genotype in five SNPs simultaneously, with up to a 100:1 signal to noise ratio. When fully developed, a single operator would be able to analyze samples at a rate of one per minute and a half, amounting to thousands per day. For malaria treatment, this translates to detailed and current knowledge of parasite resistance capabilities within a region or country, allowing governments and health ministries to effectively direct treatments, at a cost that would be feasible in the developing world.

Project Mentor: Dr. Peter Zimmerman, Global Health and Disease
Faculty Sponsor: Professor Nancy Dilulio, Department of Biology