

**LIST OF AWARD RECIPIENTS**  
**UB2020 RESEARCH AND DEVELOPMENT ACTIVITIES FUND (IRDF)**

**Corresponding Investigators  
and Co-Investigators  
November 2008**

**“Nanosensors for Neurotransmitter Detection”**

Corresponding Investigator

Frank V. Bright  
Chemistry  
College of Arts and Sciences

Co-Investigator's

Mark Swihart  
Chemical and Biological Engineering  
School of Engineering and Applied Sciences

Project Description

Neurotransmitters are the small molecules secreted by neurons that are responsible for communication between cells in the brain. Our team aims to develop new nanoscale tools that allow temporal resolution of the neurotransmitter concentration changes during the communication process on a millisecond time scale. In this way, we can examine parameters that can modulate these processes. Toward these ends, we have proposed a revolutionary sensor platform for the selective and continuous detection of acetylcholine, dopamine, epinephrine, histamine, 5-hydroxytryptamine, and norepinephrine. IRDF funding will be used to develop the first generation of these nanosensors for epinephrine (adrenaline).

**“Computational Identification of Transcription Factor Binding Sites”**

Corresponding Investigator

Marc S. Halfon  
Biochemistry  
School of Medicine and Biomedical Sciences

Co-Investigator's

Michael Buck  
Biochemistry  
School of Medicine and Biomedical Sciences

Song Liu  
Biostatistics  
Public Health and Health Professions

Program Description

Genes are regulated via the binding to DNA of proteins called transcription factors (TFs). Being able to identify the sites within the genome where specific TFs bind is thus a highly important goal for a great variety of biological and biomedical applications. Because direct

empirical solutions to this problem are frequently either not possible for technical reasons or not feasible due to constraints on time, effort, and funding, serious efforts have been made toward developing computational methods for identifying TF binding sites. The problem is complex because most TFs are able to bind not just a single DNA sequence, but rather a family of related sequences. Most methods, while having a firm theoretical footing, have not been experimentally validated in a comprehensive fashion. There is therefore no objective way to choose between competing methods; neither are there available data to illuminate in what ways current approaches fall short and to guide the development of improvements. We propose to rectify this by taking a data-driven approach to the binding site identification problem. We will (1) compile comprehensive data sets that can be used to evaluate current and future methods; (2) conduct such an evaluation of current methods; and (3) develop improved methods based on our present insights and on the results of our study.

### **“Frank Lloyd Wright's Buffalo Venture”**

#### Corresponding Investigator

Sandra Olsen  
UB Art Galleries  
College of Arts and Sciences

#### Co-Investigator

John F. Quinan  
Visual Studies  
College of Arts and Sciences

Brian Carter  
Architecture  
School of Architecture and Planning

John Edens  
University Archives  
University Libraries

#### Project Description

This traveling exhibition has its origins in UB's 1982 acquisition of the Wright-Martin Papers, an extensive body of letters, photographs, drawings, artifacts and related materials – unique in the architect's seminal prairie period -- with which it has been possible to document Wright's Buffalo venture, the twenty-four buildings and projects and the unique and closely interconnected patronage group that brought the work to fruition between 1902 and 1934.

The exhibition and catalogue will be scholarly; it will thoroughly identify and document each of the buildings and projects that resulted from Wright's involvement with Buffalo and the Larkin Company.

The theme of the exhibition is one of patronage, both the collective patronage of the Larkin executives, the persistent personal patronage of Darwin Martin over thirty years, and the transitional role of Walter V. Davidson in Wright's Broadacre City of 1932. Martin's vital role as a patron has been conspicuously overlooked by Wright scholars in favor of the post-depression era emergence of Edgar Kaufmann, Solomon R. Guggenheim, and Herbert F. Johnson.

An additional goal is that the exhibition will provide the full historical and architectural context of the Darwin D. Martin House and Graycliff, the Martin summer house. Scheduled to

open during the annual conference of the Frank Lloyd Wright Conservancy in Buffalo October 7-11, 2009, we hope the exhibition will draw attention to the richness of the legacy of Wright patronage in Buffalo and stimulate the emerging cultural tourism that is central to the region's economic recovery.

### **“Modulating Physiological Response with Novel GPCR Ligands”**

#### Corresponding Investigator

Sheldon Park  
Chemical and Biological Engineering  
School of Engineering and Applied Sciences

#### Co-Investigator's

Derek Daniels  
Psychology  
College of Arts and Sciences

#### Project Description

The kidney is critical for the maintenance of proper body fluid levels. Vasopressin, also known as anti-diuretic hormone, is a peptide that plays a key role in this regulation by interacting with a G protein-coupled receptor (GPCR) to affect water conservation by the kidney. Drugs that target vasopressin receptors have shown promise for the treatment and management of many diseases and conditions, including polycystic kidney disease, hyponatremia, congestive heart failure, diabetes insipidus, and several forms of urinary incontinence. The project funded under this award will use a novel yeast-based system to identify small molecules that interact with the vasopressin receptor. Compounds selected from the initial screen will be further tested using an animal model to evaluate their in vivo efficacy. The experiments have the potential to advance our understanding of vasopressin receptor regulation, vastly improve screening methods for small molecule-GPCR interactions, and may lead to new and improved therapeutics for the treatment of a number of kidney-related diseases and conditions.

### **“Extending a Preservation Archive through a Social Network”**

#### Corresponding Investigator

Michalis Petropoulos  
Computer Science and Engineering  
School of Engineering and Applied Sciences

#### Co-Investigator's

Thomas Slomka  
Digital Library Center  
University Libraries

#### Project Description

The Northeastern North American Indigenous Languages Archive is a new digital language archive whose goals are to preserve recordings of indigenous languages of Northeastern America and to make the data in those recordings accessible in appropriate ways to the academic community and the speaker communities whose languages are represented in the archive's

collections. The goal of the present project is to conduct research on how to form a successful pairing of the core preservation functions of the digital archive with modern social networking utilities so that the archive's collections can be effectively mobilized for research and community use. In particular, we seek to develop tools which will detect instances of content created via the social networking tools which is of sufficiently high quality to be promoted to storage in the permanent archive. For example, perhaps a speaker of a language represented in the archive will be able to provide a transcription of an untranscribed recording which would be of value to the wider community and, therefore, should be permanently preserved. Pairing digital archive technologies with social networking tools in this way represents a novel attempt to allow a kind of knowledge repository that is usually relatively static in nature to be continually improved by its users, and raises a number of interesting computational problems, including how high-quality community-generated content can be identified and how to migrate such content from the social network into the archive without breaking any links that content has to other material in the social network.

### **“Micro RNA Regulation of ABC Membrane Transporters”**

#### Corresponding Investigator

Aiming Yu  
Pharmaceutical Sciences  
School of Pharmacy and Pharmaceutical Sciences

#### Co-Investigator's

Zihua Hu  
Center for Computational Research  
Center of Excellence

Hua Zhao  
Cancer Prevention and Control  
Roswell Park Cancer Institute

#### Project Description

Drug resistance in cancer cells is one of the major obstacles for cancer therapy. Multidrug-resistance may be attributed to some membrane transporters including P-glycoprotein (Pgp), breast cancer resistance protein (BCRP) and multidrug-resistance protein 1 (MRP1) that are over-expressed in cancer cells and pump out anticancer agents from cancer cells. Understanding the regulation of these membrane transporter genes shall help overcome multidrug resistance and improve the outcomes of chemotherapy. The proposed research, therefore, aims to investigate a novel regulatory pathway, i.e. microRNA (miRNA)-controlled regulation of membrane transporter genes. Of note, miRNAs are newly-recognized, small, noncoding RNAs that govern the expression of targeted genes via the inhibition of protein synthesis and/or the cleavage of message (mRNA). To establish the feasibility of this project, we will first employ computational methods to identify possible miRNA targets in membrane transporter genes, and then explore the interaction of miRNA with drug transporter genes and, consequently, the effects on drug resistance in cancer cells. Additionally, we will explore possible genetic variations of the miRNAs and define their effects on regulation of transporter genes. The specific aims will be accomplished by effective interdisciplinary research among three faculty members, Aiming Yu, Zihua Hu and Hua Zhao at the Department of Pharmaceutical Sciences, Center for Computational Research and

Roswell Park Cancer Institute, respectively. A combination of bioinformatic, molecular pharmacological and epidemiological approaches shall be utilized.