



Géza Ambrus-Aikelin

Current position: Postdoctoral Fellow with Larry Gerace, The Scripps Research Institute, La Jolla, CA

Education: Graduate studies with Péter Zavodszky, Institute of Enzymology, Budapest, Hungary and as a visiting scientist with Robert B. Sim, University of Oxford, Oxford, U.K.; Eötvös University, Budapest, Hungary, Ph.D. in Biochemistry, 2004; Central European University, Budapest, Hungary, M.A. in Economics, 2002; Eötvös University, Budapest, Hungary, M.S. in Chemistry, 1998

Industrial work: CEO of RecomGenex, 2002–2005, Budapest, Hungary

Nonscientific interests: Snowboarding, windsurfing, squash (not the plant), hiking, photography

I am a relentless campaigner for interdisciplinary collaborations as I like to conduct research at the interface of chemical and biological sciences. In our current work we use chemical and biophysical methods, as well as cellular biology approaches to describe the first small molecule inhibitor of nuclear import. In nuclear import and export macromolecules are translocated between the cytoplasmic and nuclear subcellular compartments. I hope that our discovery will encourage other scientists to venture from the somewhat denser populated nuclear export field into the so far uninhabited chemical space of nuclear import. (Read Ambrus-Aikelin's article, DOI: 10.1021/cb100094k)



Jennifer Furman

Current position: University of Arizona, Department of Chemistry and Biochemistry, Ph.D. candidate with Prof. Indraneel Ghosh, 2005–present, expected completion September 2010; Arizona State University, B.S. in Chemistry, 2003 **Nonscientific interests:** Competitive volleyball and running, swimming, reading My research has involved the design of novel biosensors to detect a broad range of physiologically relevant biomolecules, including proteins and nucleic acids and their respective covalent modifications. This methodology relies on combining the specificity of biological recognition elements with the conditional signal generation of split-protein reassembly. In our paper we advance this technology by utilizing not only native biological recognition elements but also single chain antibody fragments to provide a general solution for the homogeneous detection of protein analytes. The use of a cell-free expression platform for production of the splitfirefly luciferase reporter allows for detection of VEGF, gp120, or HER2 in 2.5 h or less with high sensitivity. (Read Furman's article, DOI: 10.1021/cb100143m)



Image courtesy of J. M. Grant.

Daniel Grant

Current position: Investigator in Chemical Biology at GlaxoSmithKline, Research Triangle Park, NC **Education:** Burnham Institute in La Jolla, Postdoc with Nicholas Cosford, 2007–2008; University of Illinois at Chicago, Ph.D. with David Crich, 2007 **Nonscientific interests:** Running, cars, hiking I am interested in taking a nontraditional phenotypedriven approach to drug discovery. My goal is to synergistically develop chemistry and biology around compounds that have interesting biological activity, such as GSK4112. Recently, it has become increasingly evident that the resource-hungry expedition style strategy that pharmaceutical companies have adopted over the past 20 years is not sustainable. The reality that we are now facing is that the bar for the approval of new drugs and pressure on investment in preclinical drug discovery are higher than ever before. We know that in the future drug discovery will have to be leaner and smarter. While I do not know what this will look like, I'm betting that it will look more like what we are now calling chemical biology. (Read Grant's article, DOI: 10.1021/cb100141y)

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AUTHORS



Andrea Jochim

Current position: First-year medical student at Stony Brook School of Medicine

Education: New York University, M.S. in Chemistry, 2006, Ph.D. in Chemistry, 2010; Cal Poly State University, San Luis Obispo, B.S. in Biochemistry and Chemistry, 2003 **Industrial research:** Research Assistant, Santa Cruz Biotechnology Inc., 2003–2004

Nonscientific interests: Horseback riding, biking, hiking, swimming, reading books and the news

My graduate research focused on understanding molecular recognition in protein interfaces. Proteins often utilize small folded domains for recognition of each other and other biomolecules. The basic hypothesis guiding this work is that the particular function of a protein can be modulated by mimicking these folded domains with metabolically stable synthetic peptidic or nonpeptidic oligomers. The focus of the work presented in this paper was to identify protein—protein interactions that possess a helical interface and are potentially suitable candidates for inhibition by synthetic ligands. In future research I aim to incorporate experimental and computational approaches to study human health and disease. (Read Jochim's article, DOI: 10.1021/cb1001747)



mage courtesy of David H. Jaynes.

Tracy Neher

Education: Indiana University School of Medicine, Post-Doctoral in DNA Repair with Dr. John Turchi; Michigan Technological University, Ph.D. in Biochemistry with Dr. Donald Lueking, 2008; Michigan Technological University, B.S. in Biology with Dr. John Adler, 2004

Nonscientific interests: Outside of the lab I enjoy spending my time with my husband and daughter. We enjoy traveling, shopping and camping.

Our research presented in this manuscript focuses on the identification of small molecule inhibitors of xeroderma pigmentosum group A (XPA) protein via in silico screening. The SMI disrupts the XPA–DNA interaction that is necessary for efficient nucleotide excision repair (NER). We successfully targeted a direct protein-DNA interaction using XPA's predicted DNA binding domain and *in silico* modeling. Although a number of inhibitors have been identified that are capable of disrupting enzyme-substrate interactions or protein-protein interactions, few protein-DNA interactions have been targeted. This work is the first in silico targeting of a protein-DNA interaction and the next evolution in targeting macromolecule complexes. Additionally, the possibility of this SMI being used in combination treatment with common chemotherapeutics to increase efficacy may have profound effects in the clinic. (Read Neher's article, DOI: 10.1021/cb1000444)



ge courtesy of Katie Butsch.

Sarah Shuck

Education: Vanderbilt University, Postdoctoral with Lawrence J. Marnett, Ph.D.; Indiana University School of Medicine, Ph.D. in Biochemistry and Molecular Biology, Thesis Advisor, John Turchi, Ph.D.; Indiana University School of Medicine, M.S. in Physiology, Advisor, Frank Witzmann, Ph.D.; Indiana University, B.S. Biology

Nonscientific interests: Being a new resident of Nashville, TN, I have enjoyed exploring the Americana and independent rock music the city has to offer. I also enjoy being active in environmental preservation and restoration. Scientifically, my concentration is on the mechanisms of genomic maintenance and stability and its implications in cancer development and therapeutic treatment. During my graduate work at Indiana University, I focused on the development of novel small molecule inhibitors targeting proteins required for DNA repair. This work led to the discovery of a novel inhibitor of replication protein A (RPA) in addition to a class of inhibitors of xeroderma pigmentosum group A (XPA). My postdoctoral research focuses on the implications of endogenous DNA damage formed from products of lipid peroxidation. We are currently examining the chemical mechanisms of the formation of covalent protein-DNA cross-links in addition to the physiological implications of oxidative DNA damage. (Read Shuck's article, DOI: 10.1021/cb1000444)

AUTHORS



mage courtesy of Marilyne Stains.

Cliff Stains

Current position: Massachusetts Institute of Technology, Department of Chemistry, Postdoctoral Fellow with Prof. Barbara Imperiali

Education: University of Arizona, Ph.D. in Chemistry with Prof. Indraneel Ghosh, 2008; Millersville University, B.S. in Chemistry, 2002

Nonscientific interests: Music, cooking, hiking

My research is focused on developing chemical tools that address challenging biological problems. As a Ph.D. student in the Ghosh laboratory I was involved in developing split-protein sensors for the direct detection of DNA. This methodology entailed fusion of splitprotein reporter halves to separate sequence-specific DNA recognition elements. Binding of each fusion protein at appropriately spaced sites on the surface of DNA led to reassembly of the appended split-protein reporter and generation of an observable signal; we termed this technique sequence-enabled reassembly. Here we expand upon this idea of template-driven reassembly of signaling proteins by employing antibody fragments as recognition elements for the detection of biologically and clinically relevant protein targets without the need for purification or separation. (Read Stains' article, DOI: 10.1021/cb100143m)