Introducing our AUTHORS

Image courtesy of Jennifer Campbell.

Jennifer Campbell

Current position: Harvard Medical School, Department of Microbiology and Molecular Genetics, Ruth L. Kirschstein Postdoctoral Fellow with Suzanne Walker.
Education: Brigham Young University, B.S. in biochemistry, 2003; University of Wisconsin-Madison, Ph.D. in organic chemistry with Helen Blackwell, 2008.
Nonscientific interests: Running, climbing, skiing, traveling, knitting.

In recent years, we have seen a drastic rise in the frequency of bacterial infections that are resistant to antibiotics. The most frightening of these pathogens is methicillin-resistant *Staphylococcus aureus* (MRSA), which is able to survive treatment with penicillin and other β-lactams. We can no longer rely on the therapeutics of the past. In order to eradicate this growing threat to human life, we must develop new strategies that exploit novel targets. In our current paper, we report that wall teichoic acids (WTAs), phosphate-rich sugar-based polymers attached to the cell wall, are necessary for methicillin resistance in MRSA. We demonstrate that tunicamycin selectively inhibits the first step of WTA synthesis at low concentrations, and restores β-lactam sensitivity to MRSA strains. We believe that similar synthetic lethal compound combinations will constitute effective therapeutic strategies in the future. (Read Campbell's article, DOI: 10.1021/cb100269f)

Image courtesy of Scott Carlson.

Scott Carlson

Current position: Massachusetts Institute of Technology, Department of Biological Engineering and David H. Koch Institute for Integrative Cancer Research, Ph.D. candidate with Prof. Forest White.
Education: Stanford University, B.S. in chemistry, 2005; University of Cambridge, M.Phil. in computational biology, 2006.
Nonscientific interests: Tae kwon do, running, education policy.

My research focuses on how cell signaling networks are wired and particularly on the protein−protein interactions that direct kinase specificity. My aim is to develop a system-level understanding of how signaling networks change during development of disease, especially cancer. Most recently I have applied chemical genetics and proteomics to map substrates of the mitogen-activated protein kinases in a variety of biological contexts. My experiments suggest that these kinases act in a much wider range of biological processes than we had previously appreciated. To explore these new interactions I am using high-throughput sequencing and proteomics to understand the interplay between kinase signaling and other regulatory processes including histone modification, mRNA splicing, and microRNA activity. (Read Carlson's article, DOI: 10.1021/cb1002834)

Image courtesy of Sandy Lomenick.

Brett Lomenick

Current position: UCLA, Ph.D. candidate in molecular and medical pharmacology with Prof. Jing Huang.
Education: University of Tennessee at Chattanooga, B.S. in molecular biology, 2007.
Nonscientific interests: Traveling, camping, hiking, fishing, basketball, football.

I am interested in developing and using methods and technologies for finding and studying novel small molecules, both for use as chemical probes in basic biological research as well as for treatment of complex diseases. I am particularly excited about the resurgence of phenotype-based drug discovery. The major bottleneck of chemical genomics and phenotypic screening, however, is the difficulty in determining each compound's molecular targets and mechanism of action. To help overcome this obstacle, my research has primarily focused on the development of DARTS, a new method for small molecule target identification. DARTS is a unique and powerful technique that is complementary to other existing methods and should be extremely useful to chemists and biologists for identifying and studying protein-small molecule (drugs, probes, ligands, metabolites) interactions. (Read Lomenick's article, DOI: 10.1021/cb100294v)

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Image courtesy of Gavin Williams.

Gavin Williams

Current position: North Carolina State University, Assistant Professor, Department of Chemistry.
Nonscientific interests: I enjoy watching and playing 'soccer', drinking tea, live comedy and electronic music.

Throughout my career I have been interested in using enzyme engineering to produce novel biocatalysts. The work described in our paper in this issue represents the combined efforts of an extensive enzyme engineering program, resulting in the construction of a bacterial strain that harbors three mutant enzymes with sufficient substrate promiscuity to allow for the *in vivo* production of an array of glycosylated small molecules. I am now an assistant professor at North Carolina State University, where my group is applying evolutionary methods of redesign to create nucleic acids and proteins with novel functions. In particular, we are developing new strategies for screening and selecting designer nucleic acid and protein-based tools for use in chemical biology and using the power of evolution to reprogram the biosynthesis of natural products for the discovery of new drugs. (Read Williams' article, DOI: 10.1021/cb100267k)