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Tonia Buchholz

Current position: University of Michigan—Ann Arbor, Chemical Biology Doctoral Program, Ph.D. student with Prof. David H. Sherman

Education: Ohio Wesleyan University, B.A. in chemistry, 1996; University of Wisconsin–Madison, M.S. in biochemistry with Prof. Laura L. Kiessling, 2000

Industrial work: PanVera Corp., Scientist, Assays Group, 2000–2002; Rigel Pharmaceuticals, Sr. Research Associate, Immunology Group, 2002–2003; Proteolix, Inc., Scientist, Biology Group, 2004–2005

Nonscientific interests: Yoga, hiking, travel, cooking, Rilo Kiley

Fang-Yuan Chang

Current position: The Rockefeller University, Laboratory of Genetically Encoded Small Molecules, Ph.D. candidate with Prof. Sean Brady

Education: Harvey Mudd College, B.S. in joint chemistry and biology, 2007

Nonscientific interests: Snowboarding, karate, karaoke

The long-term objective of our research is to enable the design of hybrid polyketide synthase (PKS) systems for the generation of novel drug-like products with clinically relevant activities. The question of how an acyl carrier protein delivers its growing polyketide intermediate to the next domain in the pathway is answered in different ways by various PKS enzymes. In this paper, we have deconstructed the interpolypeptide junction of two type I PKS systems to investigate key protein—protein interactions. We have used both biophysical and structural approaches to obtain insights into the docking interface of these large multidomain proteins. (Read Buchholz's article, DOI 10.1021/cb8002607.)

Environmental DNA (eDNA) has great potential in providing us access to novel natural products from uncultured microbes but is inevitably restricted by the production capacity of the eDNA expression host. Our study establishes *Ralstonia metallidurans* as a novel heterologous host for the phenotypic screening of eDNA library and shows that it can produce new metabolites from genes that are not accessible by traditional hosts. We believe metagenomic studies will probably only succeed by establishing multiple phylogenetically diverse yet genetically tractable model bacterial hosts, and this study adds *R. metallidurans* onto the currently limited list of heterologous hosts for eDNA. (Read Chang's article, DOI 10.1021/cb8002754.)



ourtesy of Jeffrey Crais

mage courtesy of Fang-Yuan Chang

Jeffrey Craig

Current position: Cornell/Rockefeller/Sloan-Kettering Tri-Institutional M.D./Ph.D. candidate, performing thesis research with Prof. Sean Brady in the Laboratory of Genetically Encoded Small Molecules at Rockefeller University **Education:** Johns Hopkins University, B.A./M.A. in biophysics, 2005

Nonscientific interests: College and professional sports; watching *Comedy Central*, *House*, and *The Office*; playing with my dogs

My work in the Brady Laboratory involves exploring the broad chemical and metabolic diversity present within the genomes of uncultured soil bacteria in order to understand the chemistries and chemical evolution at work within these diverse ecosystems. By building large cosmid libraries from environmental DNA (eDNA) extracted directly from soil, we are able to find and study new bacterial pathways encoding for secondary metabolite biosynthesis. The phenotypic screening of eDNA libraries described here is greatly benefited by the use of multiple, diverse heterologous expression hosts, and represents a general strategy for identifying small-molecule-producing clones from environmental sources. (Read Craig's article, DOI 10.1021/cb8002754.)

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AUTHORS



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Tina Dasgupta

Current position: Memorial Sloan-Kettering Cancer Center, Department of Medicine, First-year Resident **Education:** University of Alberta, B.S. (Honors) in biochemistry, 2001; Yale University School of Medicine, M.D., 2008; Yale University, Ph.D. in pharmacology with Prof. Karen S. Anderson, 2008

Nonscientific interests: Hiking, oil-painting, classical piano, environmental awareness, social justice, public service, travel, salsa dancing, skiing, photography, gourmet cooking My work at the interface of chemistry and biology involves defining the molecular mechanism of clinically important enzymes at a structural and functional level. Such studies enable protein structure to be correlated with function, and can be exploited further to decipher mechanisms of disease and enhance drug discovery. My graduate project focused on a critical antimalarial drug target, thymidylate synthase-dihydrofolate reductase (TS-DHFR), mutations in whose active site have caused global resistance to antifolate antimalarial therapy. In a previous publication, we showed the importance of distant structural regions, remote from the TS-DHFR active sites, in modulating catalysis and domain-domain communication in this elegantly bifunctional enzyme. In this paper, we use a combination of computational, kinetic, and structural studies to identify a novel scaffold that is active against drugresistant malaria parasites in cell culture. (Read Dasgupta's article, DOI 10.1021/cb8002804.)



Nadine Homeyer

Current position: Friedrich-Alexander-University Erlangen-Nuremberg, Institute for Biochemistry, Ph.D. student with Prof. Sticht

Education: University of Karlsruhe, Germany, Diploma (comparable to M.S.) in biology, 2003 **Nonscientific interests:** Novels, bicycling, music

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Photo courtesy of Håvard Jenssen.

Håvard Jenssen

Current position: University of British Columbia, Vancouver, Canada, Research Associate with Prof. Dr. Robert E. W. Hancock

Education: Oslo College of Engineering, Norway, B.E. in biochemistry, 1997; University of Tromsø, Norway, C.E. in molecular biotechnology, 2000; University of Tromsø, Norway, Ph.D. in virology and peptide chemistry with Prof. Dr. Tore J. Gutteberg, 2004

Postdoctoral work: University of British Columbia, postdoc in antimicrobial peptide design, with Prof. Dr. Robert E.W. Hancock, 2007

Nonscientific interests: Mountaineering

My work in the group of Prof. Sticht focused on revealing the behavior of proteins by molecular dynamics simulations. Specifically, I have investigated the effect of post-translational phosphorylation on protein structure, function, and interactions. The implications of phosphorylation can be diverse, ranging from small, local, structural rearrangements to global changes. As demonstrated in this paper, molecular dynamics simulations can complement experimental studies in revealing the effects of phosphorylation events. It is fascinating to see how experimental findings can be explained by the information obtained from atomic level simulations based on knowledge at the intersection between physics, biology, chemistry, and informatics. (Read Homeyer's article, DOI 10.1021/cb800219m and Point of View, DOI 10.1021/cb900003f.)

Emerging infectious diseases and the escalating incidence of reported drug-resistant bacterial strains has fueled the hunt for new anti-infective drug candidates in recent years. A potential new therapeutic approach for treating infectious diseases is the use of cationic host defense peptides, also known as antimicrobial peptides. My research focuses on using sophisticated computer-aided prediction models to aid the development of novel peptide and peptidomimetic molecules that may potentially be used to treat both viral and bacterial pathogens. My work encompasses the generation of both directly antimicrobial peptides and those that do not directly kill the pathogen but instead fight infection by stimulating the host's natural innate immune system to promote the clearance of infection. (Read Jenssen's article, DOI 10.1021/cb800240j.)





Image courtesy of Ulrich Weininger.

Christian Löw

Current position: Karolinska Institutet, Department of Medical Biochemistry and Biophysics, Postdoctoral Fellow with Prof. Pär Nordlund

Education: University of Bayreuth, degree in biochemistry, 2003; University of Halle-Wittenberg, Ph.D. in biophysics with Prof. Jochen Balbach, 2008

Nonscientific interests: Traveling, table tennis, hiking, sports

My research interests during my Ph.D. have been focused on studying protein folding reactions of naturally occurring ankyrin repeat (AR) proteins. I exploit the tools of fluorescence spectroscopy, NMR, and biochemistry to characterize protein folding intermediate states and study their structure—function relationship. Folding of AR proteins seems to follow a common principle: the most stable ARs fold first and provide a scaffold for the subsequent folding of the less stable but functional repeats. In this work, we report that phosphorylation of the CDK inhibitor p19INK4d leads to unfolding of the first two ARs, whereas ARs 3-5 remain folded in this intermediate state. (Read Löw's article, DOI 10.1021/cb800219m and Point of View, DOI 10.1021/cb900003f.)