ACS chemical biology

Introducing Our Authors

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Image courtesy of Gianfranco De Pascale.

GIANFRANCO DE PASCALE

Current position: Investigator II at the Novartis Institutes for BioMedical Research, Emeryville, CA, USA.

Education: Federico II University, Italy, Laurea in Industrial Biotecnology; University of Warwick, United Kingdom, Ph.D. in Chemistry with Prof. Timothy D. H. Bugg; McMaster University, Canada, postdoctoral research fellow with Prof. Gerard D. Wright.

Nonscientific interests: Running, soccer, squash, cooking, and traveling.

My research encompasses different aspects of bacterial and fungal targets, antibiotic resistance, studying essential aspects of bacterial physiology using chemical biology approaches, and drug discovery. During my placement at Vicuron Pharmaceuticals in Dr. Stefano Donadio's research group my research was focused on the development and validation of novel assays to identify inhibitors of bacterial DNA replication and cell wall biosynthesis. My Ph.D. research was focused on studying the lipid-linked stages of peptidoglycan biosynthesis in penicillin-resistant and sensitive *Streptococcus pneumoniae*. My postdoctoral research focused on identifying and characterizing new inhibitors of bacterial and fungal metabolism and studying antibacterial resistance mechanisms. In this study we screened for and identified antibiotic adjuvants that altered cell shape and permeability in *Escherichia coli*. (Read De Pascale's article, DOI: 10.1021/cb300269g)

Image courtesy of Sang Taek Jung.

SANG TAEK JUNG

Current position: University of Texas at Austin, Department of Chemical Engineering, Research Associate with Prof. George Georgiou

Education: Seoul National University, Seoul, Korea, B.S. in Chemical Technology, 1997; Seoul National University, Seoul, Korea, M.S. in Chemical Technology, 1999; The University of Texas at Austin, Ph.D. in Chemical Engineering with Prof. George Georgiou, 2009; Postdoctoral Researcher with Prof. George Georgiou, 2009–2010; Postdoctoral Researcher with Prof. Frances H. Arnold, California Institute of Technology, 2010–2011

Nonscientific interests: Watching college football, soccer, and traveling

My work in the Dr. Georgiou group focuses on utilizing bacteria to engineer and express large quantities of human antibodies. In previous work, we have developed high-throughput screening systems and used them to isolate aglycosylated antibody Fc domains for improved therapeutic effector functions. In this work, we examine the structural impact removing the N297 glycan has on the IgG Fc domain. The N297 glycan lies in the center of the horseshoe-shaped Fc domain. As alteration or removal of this glycan can have dramatic effects on FcγR binding and in vivo efficacy, it is important to understand what structural role these carbohydrates play. Here we report a crystal structure of aglycosylated human IgG Fc domain in conjunction with in solution SAXS data. These data show significant structural differences between glycosylated, aglycosylated Fc domains, and an aglycosylated FcγRI specific Fc variant. (Read Jung's article, DOI: 10.1021/cb300130k)

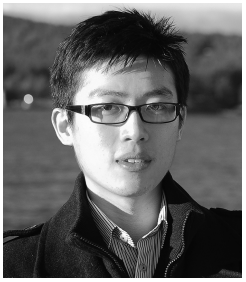

Image courtesy of Simon Ng.

SIMON NG

Current position: University of Alberta, Ph.D. candidate with Prof. Ratmir Derda in Department of Chemistry and Alberta Glycomics Centre

Education: Nanyang Technological University, B.Sc. in Chemistry and Biological Chemistry, 2010, Research advisor: Prof. Xue-Wei Liu

Nonscientific interests: Swimming, traveling, movies, and reading

My graduate research focus on developing general approaches for constructing genetically encoded and amplifiable libraries of bioactive molecules. I expand the use of phage to display and encode molecules other than natural polypeptides to make it possible to select and evolve molecules with properties not found in peptides. In the manuscript in this issue, we described a simple chemical method to convert phage-displayed peptide library into a library of glycopeptides. Such libraries are valuable sources of ligands for carbohydrate-binding proteins, bacterial

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toxins and receptors on the cell surface. We expect that this work could be expanded beyond the synthesis of library of glycopeptides and it could yield custom chemically modified phage libraries of large structural complexity. (Read Ng's article, DOI: 10.1021/cb300187t)

Image courtesy of Karen E. Gross.

PIA SÖRENSEN

Current position: Harvard University, School of Engineering and Applied Sciences, Preceptor in Science & Cooking.

Education: Yale University, B.S. in Molecular Biophysics and Biochemistry, 2005; Harvard University, Ph.D. in Chemical Biology with Prof. Ulrike Eggert, 2011

Nonscientific interests: Interdisciplinary applications of science, yoga, art, food, painting, literature, nature

My research in the Eggert lab focused on understanding the target and mechanism of cucurbitacin E, a small molecule that we isolated from plant extract after it scored positive in a screen for small molecule inhibitors of cell-division. The work presented in this paper describes how cucurbitacin E acts by a unique mechanism on actin, and compares it to that of another common actin binder, jasplakinolide. Cucurbitacin E is a widely available natural product, making it a useful tool to study actin dynamics in cells and actin-based processes. More recently, I have been pursuing work related to my interest in interdisciplinary applications of science. As an educator in the science of food and cooking, I hope to bring creative and intuitive approaches to science education that promotes awareness of the physics and chemistry everywhere around us. (Read Sorensen's article, DOI: 10.1021/cb300254s)

Image courtesy of David Eng.

PATRICIA TAYLOR

Current position: Scientific Evaluator, Health Canada

Education: University of Guelph, Canada, B.Sc. in Biochemistry, 2004; McMaster University, Canada, Ph.D. in Biochemistry with Gerard D. Wright, 2011

Nonscientific interests: Reading, movies, and baseball

My graduate research at McMaster University focused on identifying and characterizing potential targets for novel antibiotic therapies to combat infections caused by Gram-negative pathogens. This work included enzymology, structural biology, chemical biosynthesis and high-throughput screening applications. Previous efforts included structure–function analysis of the GmhA and GmhB enzymes in the lipopolysaccharide biosynthetic pathway. In this paper, we screened 30 000 small molecules to identify antibiotic adjuvants of novobiocin, an aminocoumarin antibiotic, in *Escherichia coli*. From this screen we identified four compounds with adjuvant activity, all of which were associated with altered cell shape. Targets included the bacterial cytoskeleton protein MreB, cell wall biosynthesis enzymes and DNA synthesis. This research suggests that inhibitors of cell shape have the potential to be developed into novel combination therapies for infections caused by Gram-negative bacteria. (Read Taylor's article, DOI: 10.1021/cb300269g)

Image courtesy of Yu Zeng.

YU ZENG

Current position: Texas A&M University, Department of Chemistry, Postdoctoral Research Associate with Dr. Wenshe Liu

Education: Sichuan University, Chengdu, China, M.S. in Biochemistry with Prof. Mingshan Liang, 1996; Ph.D. in Botany with Prof. Fang Chen, 2003; Associate Professor in Biochemistry and Molecular Biology, 2003–2009; Postdoctoral research fellow in Institute of Molecular and Cellular Biosciences, the University of Tokyo, Japan, with Prof. Kan Tanaka, 2005–2007; Postdoctoral research fellow in Department of Biological Sciences, Ohio University, with Prof. Shawn Chen, 2007–2011

Nonscientific interests: Hiking, fishing, and music

My postdoctoral work at the University of Tokyo focused on RNA polymerase sigma factor for the bacterial transcription regulation and chloroplast differentiation. At Ohio University, we focused on biosynthesis of microbial complex secondary metabolites on novel moleculars for anticancer and anti-infective drugs in *Streptomyces*. In this article, we reported the identification of the gene cluster for Trojan horse albomycin production and a related biosynthetic gene cluster from another *Streptomyces* sp. C strain, elucidated the mechanisms for installing the chemical features found in albomycins, which provide a biosynthetic template for assembling siderophore-inhibitor conjugates and modifying the albomycin scaffold to generate new derivatives. Since 2011, I started research at Texas A&M University on phage and bacteria display with two genetically incorporated noncanonical amino acids to expand the chemical diversity and select novel peptide drugs by high throughput screening against cancer therapeutic targets. (Read Zeng's article, DOI: 10.1021/cb300173x)