ACS chemical biology

Introducing Our Authors

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Image courtesy of Karan Bhuripanyo.

KARAN BHURIPANYO

Current position: Graduate student research assistant in Prof. Jun Yin's lab, Department of Chemistry, University of Chicago

Education: Baylor University, B.S. in Biochemistry, 2009; University of Chicago, M.S. in Chemistry (organic), research advisor: Jun Yin, 2011

Nonscientific interests: Classical piano, musical composition, East Asian pop culture, chess, good food!

Currently, I am assisting Prof. Yin in the design of an orthogonal ubiquitin transfer pathway, with a particular emphasis on the E2-E3 interface. Our results suggest that E1 enzymes display a surprising level of flexibility in accommodating a variety of different C-terminal sequences in ubiquitin; this may suggest that E2, and perhaps E3 enzymes as well, possess ubiquitin-recognizing-domains that have more stringent requirements for specificity. Interestingly, most E3 enzymes are of RING type, which in the presence of substrate proteins are never covalently linked to ubiquitin and are thought of as merely bridges between the E2 and substrate. Considering that there are only several dozen E2 enzymes, as opposed to thousands of E3 enzymes, the mechanism by which the cell is able to precisely control the ubiquitination of and hence regulate the lifespan of its countless number of proteins makes for an intriguing subject of study. (Read Bhuripanyo's article, DOI: 10.1021/cb300339p)

Image courtesy of Karl Brillet.

KARL BRILLET

Current position: Academic engineer position at CNRS, preparing a Ph.D. in the lab of Dr. Isabelle Schalk, CNRS–Strasbourg University, UMR7242, Biotechnology and Cell Signaling unit

Education: University of Caen-Basse Normandie, France, Master in Biochemistry, 1999

Nonscientific interests: Motorbike, trek, movies, theater, music

Iron is an essential element for bacterial growth during infection, and thus understanding the molecular mechanism involved in iron acquisition is a way to identify new antimicrobial targets. In the past years, I performed functional and structural studies of TonB-dependent transporters in Gram-negative bacteria. My project is now focused on the ferrisiderophore transport in *Pseudomonas aeruginosa*, a mutiresistant, Gram-negative bacteria involved in cystic fibrosis. Recently, we identified an inner membrane protein complex FpvCDEF involved in the iron uptake through the pyoverdine pathway. Our studies show that FpvCDEF complex is an ABC transporter with the particularity of having two periplasmic binding proteins FpvC and FpvF. Our experiments highlight complexes formation between FpvC and FpvF, able to bind pyoverdine or pyoverdine-iron. In the future, we will focus on this complex, probably implicated in the ferrisiderophore dissociation process. (Read Brillet's article, DOI: 10.1021/cb300330v)

Image courtesy of Jennifer McCarthy.

JENNIFER MCCARTHY

Education: University of Maryland, College Park, B.S. in Biochemistry and B.A. in Music, 2007, Advisor: Steve Rokita; University of Michigan, Ph.D. in Biological Chemistry, 2012, Advisor: Janet L. Smith

Nonscientific interests: Playing the clarinet, reading, cooking

Natural product biosynthetic pathways, such as polyketide synthases, are an abundant source of rare and unusual enzymes synthesizing interesting functional groups. My Ph.D. work

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focuses on one such functional group, a terminal alkene, from the curacin A biosynthesis pathway. A sulfotransferase (ST) sulfonates a β-hydroxy substrate and a thioesterase (TE) catalyzes a sulfonation-assisted decarboxylation to generate the terminal alkene. The discovery of the ST-TE domains in the hydrocarbon-producing olefin synthase opens the door to using this system for biofuel production. The paper presents the study of the curacin and olefin synthase ST domains, which have an unusual role in leaving-group activation, a role typical for phosphorylating enzymes but not for sulfotransferases. (Read McCarthy's article, DOI: 10.1021/cb300385m)

Image courtesy of Michael Vetter.

MICHAEL VETTER

Current position: Harvard Medical School, Microbiology and Immunobiology, Postdoctoral Research Fellow, Advisor: Dr. Priscilla L. Yang

Education: Case Western Reserve University, B.A., Biology, 1999; Vanderbilt University Medical Center, Ph.D. in Microbiology and Immunology, advisor Dr. Richard T. D'Aquila, 2009

Nonscientific interests: Hiking, reading history, movies, cooking

I am interested in identifying host effectors of viral replication that may be targeted to inhibit viral pathogens. Currently, I apply those interests to dengue virus. The goal of our study was to identify changes in host enzymes that occur on a time scale shorter than transcription or translation. Using ATP- and ADP-acyl phosphates as chemical probes we were able to interrogate changes in the host kinome within 1 h of dengue infection. This profiling uncovered a novel role of DNA dependent protein kinase (DNA-PK) specific to dengue virus infection. Generally this work describes a unique way to examine the effects of viral infection on a host cell and more specifically implicates a new host factor in the cellular response to dengue virus infection. (Read Vetter's article, DOI: 10.1021/cb300420z)

BO ZHAO

Current position: Postdoctoral fellow in Jun Yin's lab at the Department of Chemistry of the University of Chicago

Education: Jilin University, B.S. in Biochemistry, 2002; M.S. in Biochemistry and Molecular Biology, 2005, Research advisor: Yingjiu Zhang; Ph.D. in Biochemistry and Molecular Biology, 2009, Research advisor: Shugui Cao

Nonscientific interests: Running, tennis, chess, soccer, traveling, movies, cooking, swimming

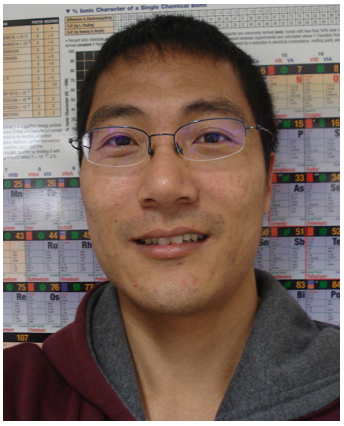

Image courtesy of Bo Zhao.

My current research is to engineer ubiquitin (UB) and ubiquitin-like proteins (UBLs). As described in our manuscript, we developed a phage display method to identify UB mutants that can form polymers resistant to the cleavage reactions of deubiquitinating enzymes (DUB). Our results also revealed that the E1-E2-E3 cascade reads the highly conserved C-terminal sequence of UB to give it the green light to pass through the cascade. Currently I am developing short peptides that can be loaded on the cascade enzymes as the full length UB based on our phage selection results. Furthermore I am interested in using phage display to engineer UBL proteins important for cell signaling including Nedd8, SUMO and ISG15, etc. (Read Zhao's article, DOI: 10.1021/cb300339p)