# Introducing our AUTHORS

**Zhe Zhou**

**Current position:** Harvard Medical School, Department of Biological Chemistry and Molecular Pharmacology, Ph.D. candidate with Prof. Christopher T. Walsh
**Education:** Tsinghua University, China, B.S. in biological science, 2004
**Nonscientific interests:** Traveling, sailing, table tennis, charity

My research focuses on the use of directed evolution to characterize and reprogram protein–protein interactions. I have applied selections and screens to study the carrier protein domains to which substrates are covalently tethered during fatty acid, polyketide, and nonribosomal peptide biosynthesis. I have been particularly interested in the interaction between phosphopantetheinyl transferases (PPTases) and carrier proteins because PPTases can be used for protein labeling. We developed 12-residue peptides that mimic carrier proteins by serving as orthogonal substrates for the PPTases Sfp and AcpS. These genetically encoded peptide tags allow us to label two proteins specifically with different small molecules on the surface of a single cell. (Read Zhou's article on p 337.)

**Pablo Cironi**

**Current position:** Harvard Medical School, Department of Systems Biology, Postdoctoral Fellow in Prof. Pamela Silver's group
**Education:** University of Buenos Aires, School of Exact and Natural Science, B.S. in chemistry, 2000; University of Barcelona, Ph.D. in organic chemistry with Profs. Fernando Albericio and Mercedes Alvarez, 2004
**Nonscientific interests:** Spending time with friends, traveling, hiking. I also like wine tasting and preparing asados.

My interests are in drug development, discovery, and delivery. I have used synthetic chemistry approaches for the discovery of new molecules, but I recently transitioned to a systems biology approach. My current work focuses on the design and expression of novel proteins that specifically target cells overexpressing epidermal growth factor receptor. Using a rational synthetic approach, we computationally modeled fusion proteins that target specific tumor cells. A product of a collaboration related to my current work, the report published here describes the use of genetically encoded peptide tags that allow us to orthogonally label and study the interaction between two different receptors. (Read Cironi's article on p 337.)

**Alison J. Lin**

**Current position:** Harvard Medical School and Brigham and Women's Hospital, Depts. of Medicine and Biol. Chemistry, Molec. Pharmacology, Instructor
**Education:** Univ. of Minnesota–Twin Cities, B.S. in physics, 1993; Univ. of California–Santa Barbara, Ph.D. in physics with Prof. Cyrus Safinya, 2001
**Postdoctoral work:** Harvard Medical School with Profs. David E. Golan and Thomas Michel, 2001–2006
**Nonscientific interests:** Music, good books, yummy food, badminton, Star Trek

I study molecular interactions involved in membrane receptor-mediated signaling. Direct imaging of proteins in living cells allows real-time monitoring of protein distribution, activity, and interaction with other proteins. I have applied confocal microscopy and FRET techniques to explore the dynamics of proteins in nitric oxide signaling pathways in vascular endothelial cells. Successful imaging applications require efficient and specific labeling of proteins in the cellular environment. We demonstrated here orthogonal labeling of two different proteins in the same living cell. This holds great potential for applications in protein visualization. Using advanced molecular-scale imaging techniques coupled with novel protein-labeling technology, I hope to improve our understanding of complex intracellular signaling pathways. (Read Lin's article on p 337.)

**Ratmir Derda**

**Current position:** University of Wisconsin–Madison, Department of Chemistry, Ph.D. candidate with Prof. Laura Kiessling
**Education:** Moscow Institute of Physics and Technology, Russia, B.S. in physics, applied mathematics, and biophysics, 2001
**Nonscientific interests:** Music, from classical (opera) to electronic (DJ for house parties and local clubs), contemporary art, skiing

Embryonic development is one of the most amazing examples of the emergence of an extremely complex system from a relatively simple one. The analysis of development has reached an incredible degree of sophistication. Yet, we are still unable to synthesize and re-create the environment to imitate the way nature organizes complex biological systems. I am developing methods for the fabrication of multicomponent molecular arrays to study long-term cell behavior. With this technique, we can re-create hundreds of extracellular environments on one chip and rapidly identify the substrates that have a desired effect on cells (growth or differentiation). Our array strategy can be used to discover synthetic substrates that support the growth and self-renewal of human embryonic stem cells. (Read Derda's article on p 347.)

**Lucy M. Elphick**

**Current position:** Imperial College, London, Department of Cell and Molecular Biology, Postdoctoral Research Associate with Dr. David J. Mann
**Education:** University of Surrey, U.K., B.Sc. in biochemistry, 2002; University of Surrey, Ph.D. in biochemistry with Drs. George E. N. Kass and Nick J. Toms, 2005
**Nonscientific interests:** Food, music, the 2007 London Triathlon

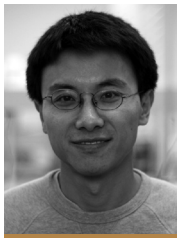
My research interests lie in the identification of novel cell cycle kinase substrates. We have brought together current work that uses chemical genetics to study protein kinases. I know it is important to retain specificity when inhibition assays are used to study enzyme function. Current small-molecule inhibitors of kinases do not always offer this specificity; however, chemical genetics techniques discussed in this review show that altering the enzyme to accept an unnatural ATP analogue allows us to dissect the specific substrate libraries and functions of individual kinases. The identification of novel cyclin kinase substrates will give us useful insights into the workings of the cell cycle and may also help to identify potential anticancer drug targets. (Read Elphick's article on p 299.)

**Published online May 18, 2007 • 10.1021/cb700095p CCC: $37.00**

**Sarah E. Lee**

**Current position:** Oxford University, U.K., Chemistry Research Lab, Postdoctoral Research Associate with Drs. V. Gouverneur and D. Mann
**Education:** University of Bangor, Gwynedd, North Wales, Ph.D. in synthetic organic chemistry with Dr. P. J. Murphy, 1998
**Postdoctoral work:** Krebs Institute, Sheffield University, U.K., Postdoctoral Research Associate under Drs. J. A. Grasby and D. M. Williams; Oxford University, U.K., Postdoctoral Research Associate under Prof. B. G. Davis. I worked at Solexa, a company founded by S. Balasubramanian and D. Klenerman.

My understanding of molecular biology is that it is the study of the interconnections between the nucleic acids and proteins, whereas chemical biology is more the study of cellular processes by unnatural interactions. The family of kinase enzymes is huge, and it is extremely important in terms of cell signaling and processing. As such, the elucidation of kinase substrates and signaling pathways remains one of the major challenges in molecular biology and, as this review illustrates, one that lends itself well to the chemical biology approach. ATP analogues have a major role to play in answering these questions. The interdependence of chemistry and biology (and chemists and biologists!) in the design of second-generation analogues is inherent, and the effective design and synthesis of new and varied second generation ATP analogues will be necessary if we are to fully answer these questions. (Read Lee's article on p 299.)



**Jinhua Chen**

**Current position:** Forbes Medi-Tech Research, Inc., La Jolla, CA, Research Scientist
**Education:** University of Science and Technology of China, Beijing, B.S. in chemical physics, 1997; University of Maine, M.S. in chemistry with Prof. Mitchell Bruce, 1999; Purdue University, Ph.D. in medicinal chemistry with Prof. Mark Cushman, 2004
**Postdoctoral work:** Burnham Institute for Medical Research with Prof. Maurizio Pellecchia, 2004–2007
**Nonscientific interests:** Travel, outdoors, photography

We wanted to test whether fragment-based screening by NMR could be effective in identifying compounds that bind selectively to the inactive form of the protein kinase p38a. We sought to combine NMR experimental data with simple 2D pharmacophore searches based on discovered scaffolds to select commercially available compounds for testing. This approach could be a very attractive alternative to high-throughout screening (HTS). Unfortunately, HTS often identifies compounds with undesirable properties. For example, we have also screened a commercial library of 14,000 compounds, using an HTS fluorescence displacement assay. We found that this HTS campaign identified hits that are nonspecific "frequent hitters" and/or promiscuous protein aggregators. Hence, our fragment-based approach provided compounds that are superior to those obtained by a typical HTS approach. (Read Chen's article on p 329.)

**Grant D. Geske**

**Current position:** University of Wisconsin–Madison, Department of Chemistry, Ph.D. candidate with Prof. Helen E. Blackwell
**Education:** St. Norbert College, B.S. in chemistry, 1998; Utah State University, M.S. in computational chemistry, 2001
**Nonscientific interests:** Spending time with my wife and three children, bicycling, listening to music

My research has centered on the design, synthesis, and evaluation of small molecules that modulate quorum sensing in bacteria. Chemical biologists have a unique opportunity to expand the current understanding of how these complex bacterial cell–cell signaling networks work. Such research will also advance our understanding of host–bacteria interactions, which include important symbioses and pathogenic relationships. Quorum sensing may represent a new target for anti-infectives. Our article focuses on the Gram-negative symbiont *Vibrio fischeri* and the discovery of what we believe to be the first quorum sensing superagonist in this bacterium. Elucidating this ligand's mechanism of action and applying it *in vivo* are some of our group's current goals. (Read Geske's article on p 315 and Point of View p 293.)

**Yan Zhang**

**Current position:** Salk Institute for Biological Studies, Jack Skirball Center for Chemical Biology and Proteomics, Postdoctoral Fellow in Prof. Joseph P. Noel's group
**Education:** Tsinghua University, China, B.S. in chemistry, 1997; University of Oregon, M.S. in chemistry with Prof. Brian W. Matthews, 2000; the Scripps Research Institute, Ph.D. in molecular biology with Prof. Ian A. Wilson, 2004
**Nonscientific interests:** Traveling, gourmet cooking, reading ancient Chinese literature

I have always been amazed by the complexity of oncogenic signaling pathways and their versatility in biological regulation. I also am very interested in structure-aided inhibitor design. The target molecule of my research, human Pin1, represents a unique way of post-translational regulation that has been exploited by tumor cells to divide and prosper. Pin1 can amplify oncogenic signaling by changing the conformation of phosphorylated proteins. In this study, we determined the high-resolution structures of Pin1 complexed to high-affinity peptide inhibitors of the Pin1 prolyl peptide isomerase domain. These structures serve as starting points for a new direction in Pin1 inhibitor design. (Read Zhang's article on p 320.)