acs chemical biology

Introducing our AUTHORS

Jemy A. Gutierrez

Current position: Yeshiva University, Albert Einstein College of Medicine, Postdoctoral Researcher with Prof. Vern L. Schramm
Education: University of the Philippines, B.S. in chemistry with Prof. Virginia D. Monje, 1997; University of Florida, Ph.D. in chemistry with Prof. Nigel G. J. Richards, 2006
Nonscientific interests: Performing arts, travel, movies, badminton

Some of the most powerful enzyme inhibitors have arisen from a deeper understanding of transition states and from capturing critical features in stable analogues. What's fascinating is seeing the power of kinetic isotope effects in action, in revealing chemical subtleties within the picosecond lifetime of transition states, and, hence, in generating potent inhibitors that are currently undergoing clinical evaluation. Here, we extend our work on inhibitor design based on transition state structure, in showing that, inversely, the K_d ratio for a pair of analogues that mimic two states in the reaction coordinate has predictive value for determining the transition state structure. (Read Gutierrez's article on p 725 and Point of View on p 711.)

Minkui Luo

Current position: Yeshiva University, Albert Einstein College of Medicine, Department of Biochemistry, Postdoctoral Researcher with Prof. Vern L. Schramm
Education: Fudan University, China, B.S. in chemistry, 1999; Princeton University, Ph.D. in chemistry with Prof. John T. Groves, 2005
Nonscientific interests: Tennis, swimming, fishing

My graduate work involved the synthesis and characterization of bacterial siderophore amphiphiles. These molecules contain hydrophilic iron-chelating moieties and hydrophobic chains, and therefore both chelate iron and interact with membranes. My research was aimed at understanding the two processes at molecular levels. The focus of my postdoctoral research is to elucidate the transition state structures of biologically essential enzymes. My short-term career goal is to launch a research team as an independent investigator. My long-term commitment in biomedical research is to continue exploring fundamental biological processes by using the tools at the interface of chemistry and biology. (Read Luo's article on p 725 and Point of View on p 711.)

Jeremy O. Jones

Current position: University of California, San Francisco, Department of Neurology, Postdoctoral Fellow with Marc I. Diamond, M.D.
Education: Pennsylvania State University, B.S. in microbiology with Prof. Richard J. Frisque, 2000; Stanford University, Ph.D. in microbiology and immunology with Ann M. Arvin, M.D., 2005
Nonscientific interests: Pittsburgh Steelers football, home-brewing, biking

I am interested in creating disease models that accurately reproduce a molecular event in a disease process and can be used for high-throughput screening to discover new treatments for disease. Our review highlights the importance of such systems, how to design them, and how to facilitate the translation of hits into clinical treatments. Recently, I have applied this strategy to finding novel inhibitors of the androgen receptor and treatments for prostate cancer. In the future, I plan to do the same for latent DNA viruses and the diseases they cause in humans. (Read Jones's article on p 718.)

Jose L. de Paz

Current position: Chemical Research Institute (IIQ), CSIC, Sevilla, Spain, Postdoctoral Fellow with Dr. Pedro M. Nieto
Education: University of Sevilla, Spain, B.S. in chemistry, 1996; Chemical Research Institute (IIQ), CSIC, Sevilla, Spain, Ph.D. in organic chemistry with Prof. Dr. M. Martín-Lomas and Dr. J. M. Lassaletta, 2000
Postdoctoral work: Swiss Federal Institute of Technology (ETH), Laboratory for Organic Chemistry, Zurich, Switzerland, with Prof. Dr. Peter H. Seeberger, 2004–2007
Nonscientific interests: Music, history, reading, watching movies

Heparin and heparan-sulfate glycosaminoglycans (HSGAGs) participate in a wide variety of biological processes, including cell growth, viral infection, and inflammation, by interacting with a host of proteins. My Ph.D. work was focused on the chemical synthesis of heparin oligosaccharides as basic tools for unraveling the role of these complex biopolymers. My postdoctoral work gave me additional opportunities to further explore interactions of HSGAGs and various signaling proteins. We developed a method for the preparation of microarrays displaying synthetic heparin oligosaccharides. In the current paper, we characterize the heparin-binding profile of several chemokines, a family of proteins that control the selective trafficking of leukocytes, by using these microarrays. Our contribution to the understanding of HSGAG–chemokine interactions is the first step toward the design of novel drugs that modulate chemokine activity as exemplified by the use of dendrimers coated with synthetic heparin sequences to inhibit lymphocyte migration. (Read de Paz's article on p 735.)

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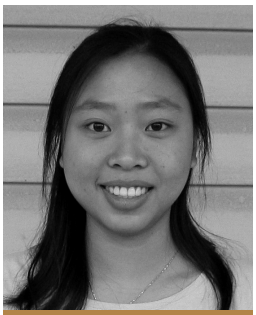
Jessica L. Childs-Disney

Current position: Canisius College, Department of Chemistry & Biochemistry, Assistant Professor
Education: Messiah College, B.S. in chemistry, 1998; University of Rochester, M.S. in chemistry, 2000; University of Rochester, Ph.D. in chemistry with Prof. Douglas H. Turner, 2003
Postdoctoral work: Swiss Federal Institute of Technology Zurich (ETH), Laboratory for Organic Chemistry with Prof. Peter H. Seeberger, 2003–2005; The State University of New York at Buffalo, Department of Chemistry with Prof. Matthew D. Disney, 2005–2006
Nonscientific interests: Traveling, spending time with family

My research interests center on the interesting structures that RNA adopts. Though RNA is chemically similar to DNA, it folds into complex 3D structures like proteins do. Its ability to adopt a variety of 3D structures allows it to perform diverse biological roles such as regulation of gene expression and catalysis. RNA's structural diversity also makes it difficult to rationally design drugs or probes of function. One way to rationally design probes would be to first understand how ligands interact with simple RNA motifs. Once enough RNA motif–ligand partners are cataloged, the information could be used to target biologically interesting RNAs. Our article describes a method for identifying the RNA motifs that a ligand prefers. In particular, we found that 6′-*N*-5-hexynoate kanamycin A prefers to bind internal loops that present an adenine across from a cytosine. (Read Childs-Disney's article on p 745.)



Meilan Wu

Current position: The State University of New York at Buffalo, Department of Chemistry, Senior Undergraduate
Education: The State University of New York at Buffalo, currently pursuing a B.S. in medicinal chemistry; undergraduate research with Dr. Matt Disney, 2006 to present
Nonscientific interests: Music, traveling, reading Chinese novels

It has been known for a long time that aminoglycosides can bind to bacterial ribosomal RNA and inhibit protein synthesis. The alternative RNA structures, including secondary structures, that these compounds bind, however, are poorly defined. During my undergraduate research with Dr. Disney, I have synthesized a series of azido-aminoglycosides and selected the RNA internal loops that they bind by using our microarray-based selection method. We hope that this information will offer a better understanding of how to target RNA with small molecules. (Read Wu's article on p 745.)

Alexei Pushechnikov

Current position: The State University of New York at Buffalo, Department of Chemistry, Postdoctoral Scholar with Prof. Matthew D. Disney
Education: Institute of Chemical Technology, Dnepropetrovsk, Ukraine, B.S. in chemical engineering, 1994; Kiev Polytechnic Institute, Ukraine, M.S. in chemical engineering, 1996; Research Institute of Organic Chemistry, National Academy of Sciences of Ukraine, Ph.D. in organic chemistry with Prof. Andrey A. Tolmachev, 2000
Postdoctoral work: University of Wisconsin–Madison, Department of Chemistry, with Prof. Howard E. Zimmerman, 2003–2006
Nonscientific interests: Handcrafting

I am interested in the development of new diversity-oriented synthetic methodologies for obtaining small-molecule libraries as well as screening the latter against various biological targets. Although RNA's importance as a target for drug development has long been acknowledged, practical application remains a challenge, mainly because of the limited quantitative structure–activity relationship data available on RNA–ligand interactions for piloting rational design. An agarose microarray platform has proven to be an excellent tool for successfully merging nucleic acid selection and small-molecule screening. A combinatorial approach to the modification of ligands with surface-specific linkers offers a deeper insight into the governing principles of the binding mode. (Read Pushechnikov's article on p 745.)