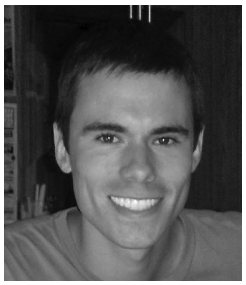

Image courtesy of David Bryson.

DAVID I. BRYSON

Current position: Virginia Tech, Ph.D. Candidate in Chemistry; Research advisor, Webster L. Santos

Education: University of North Carolina at Greensboro, B.S. Biochemistry, 2005; M.S. Biochemistry, 2007

Nonscientific interests: Music, art, guitar, exercise, and cooking

My Ph.D. research has focused on the design of branched peptides as ligands for RNA structures that are critical to the HIV life cycle. The HIV-1 transactivation response element (TAR) and the HIV-1 rev response element (RRE) have been of particular interest in my research for their critical roles in transcription, splicing, nuclear export, and translation of the viral RNA. Because our peptides feature an unnatural branch, they can form strong multivalent interactions with the three-dimensional RNA structure, yet they are small enough to be cell-permeable. We are excited by our results because RNA targeting is a complex problem that has huge potential medicinally and as a tool for biotechnology. (Read Bryson's article, DOI: 10.1021/cb200181v)

Image courtesy of Kelly Parker.

STEVE PARKER

Current position: Pharmacology Research Associate (PRAT) Fellow at NIGMS, Genome Technology Branch at NHGRI, National Institutes of Health. Previous Advisor: Dr. Elliott Margulies. Current Advisor: Dr. Francis Collins.

Education: East Carolina University, B.S. Biology and M.S. Molecular Biology; Advisor, Dr. Edmund Stellwag; Boston University, Ph.D. Bioinformatics; Advisor, Dr. Thomas Tullius

Nonscientific interests: Soccer, cycling, hiking, tea, music, art, motorcycles, auto racing, Boston Red Sox, outings with my wife and our dogs

My general scientific interests encompass understanding how functional information is encoded in the noncoding portion of genomes. I rely on computational methods that use comparative and functional genomics to address this question. The work we report here is a perfect reflection of my interests. I think the paper is appealing because it integrates chemistry, biology, and computational approaches to decipher noncoding signals. We first demonstrate the feasibility of producing DNA shape maps for entire genomes and then use these maps to show that shape is linked to nucleosome positioning. There's certainly more shape-based signals encoded in genomes, and I'm excited to continue the search! (Read Parker's article, DOI: 10.1021/cb200155t)

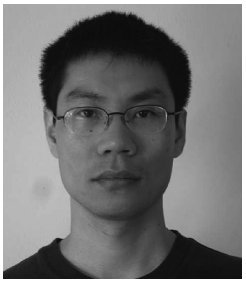

Image courtesy of Qianli Wang.

QIANLI WANG

Current position: Research Chemist at Synchem, Inc.

Education: Shenyang Pharmaceutical University, China, B.S. in Pharmaceutics, 1996; Ph.D. in Medicinal Chemistry, 2003.

Nonscientific interests: Movie, music, fishing.

My Ph.D. research was focused on the total synthesis of natural glycoconjugates with antitumor activities. While working as a research associate in Prof. Zhongwu Guo's laboratory at Wayne State University, my main research interest was to develop novel cancer immunotherapies based on joint applications of synthetic vaccines made of artificially modified sialyl tumor associated carbohydrate antigens (sialo-TACAs) and metabolic engineering of sialo-TACAs on cancer cells. In the process, we explored a new construct of fully synthetic vaccines that had TACAs coupled to monophosphorylated lipid A and proved that the resultant vaccines were self-adjuvanting

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and provoked desirable IgG antibody responses in the mouse. (Read Wang's article, DOI: 10.1021/cb200358r)

Image courtesy of Liqun Xia.

LIQUN XIA

Education: Zhejiang University of Technology, B.S. Bioengineering, 2008; Zhejiang University, Ph.D. Candidate in Pharmaceutical Chemistry; Research Advisor, Prof. J. Stöckigt

Nonscientific interests: Sports, traveling, and film

My research at Zhejiang University focused on the kinetic analysis and 3D structure elucidation of a plant enzyme Raucaffricine Glucosidase (RG). RG catalyze a side route reaction of the antiarrhythmic ajmaline biosynthetic pathway and is the second glucosidase presented in the same biosynthetic network. The two similar glucosidases in *Rauvolfia serpentina*, however, have evolved to catalyze two distinct reaction and exhibit quite different substrate specificities. X-ray analysis of RG, especially its substrate complex, provides an explanation as to the different functional behavior of each of these enzymes. (Read Xia's article, DOI: 10.1021/cb200267w)

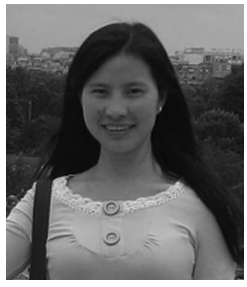

Image courtesy of Yeyun Zhou.

YEYUN ZHOU

Current position: Cornell University, Field of Biophysics, Graduate student with Prof. Richard A. Cerione

Education: University of Science and Technology of China, B.S. in Biological Sciences, 2005

Nonscientific interests: Aromatherapy, soap-making, fishing, and family

My research interest focuses on the structure–function studies of enzymes and signaling molecules for structure-based drug design. In our current paper, I solved the complex structures of a sirtuin homologue in *Plasmodium falciparum*, PfSir2A. The structures provided insights into PfSir2A's novel enzymatic activity that PfSir2A preferred to remove the long chain fatty acid modification from substrate lysine. PfSir2A, cooperating with PfSir2B, has been shown to regulate the mutually exclusive expression of surface antigen to evade the host immune surveillance. Since *Plasmodium falciparum* is a most dangerous specie that causes malaria, the structures will benefit the design of specific inhibitors of PfSir2A for potential therapeutic application. (Read Zhou's article, DOI: 10.1021/cb200230x)

Image courtesy of Zhifang Zhou.

ZHIFANG ZHOU

Current position: Wayne State University, graduate student pursuing Ph.D. at Department of Chemistry, under the supervision of Dr. Zhongwu Guo

Education: University of Science and Technology of China, Anhui, China, B.S. in Chemistry, 2009.

Nonscientific interests: Outdoor sports, social service, traveling

My Ph.D. research is focused on the development of novel cancer immunotherapies based on metabolic engineering of tumor-associated carbohydrate antigens (TACAs) on the cancer cell surface. At present, I am working on the development of methods for analyzing TACAs expressed by cancer cells and *in vitro* and *in vivo* studies of the new cancer immunotherapy. Metabolic engineering of sialo TACAs on cancer cells can be achieved by giving cells an unnatural derivative of *N*-acetyl-D-mannosamine as a sialic acid and sialo TACA biosynthetic precursor, allowing cancer cells to express TACAs carrying artificial sialic acid residues. The resultant unnatural TACA derivatives are useful templates for the design and development of functional cancer vaccines. For this research, it is important to have efficient and reliable methods for the evaluation of unnatural sialic acids and sialo TACAs expressed by cancer cells both *in vitro* and *in vivo* and to identify the optimal precursors and treatment schemes for the new cancer immunotherapy. It is also important to have vaccines that can provoke T cell-mediated immune responses and IgG antibodies. In this work, we explored a new vaccine construct that had TACAs coupled to monophosphorylated lipid A and proved that the resultant fully synthetic vaccines, which possessed well-defined structures, were self-adjuvanting and provoked desirable IgG antibodies. (Read Zhou's article, DOI: 10.1021/cb200358r)