ACA RefleXions

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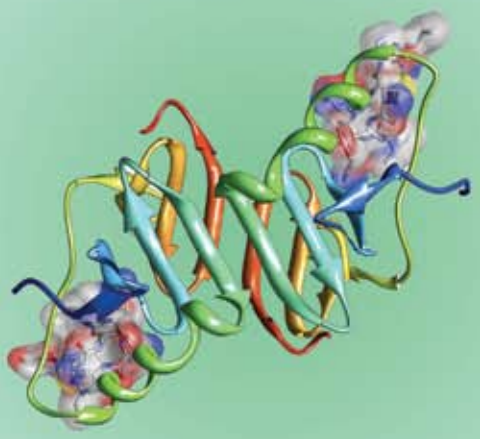
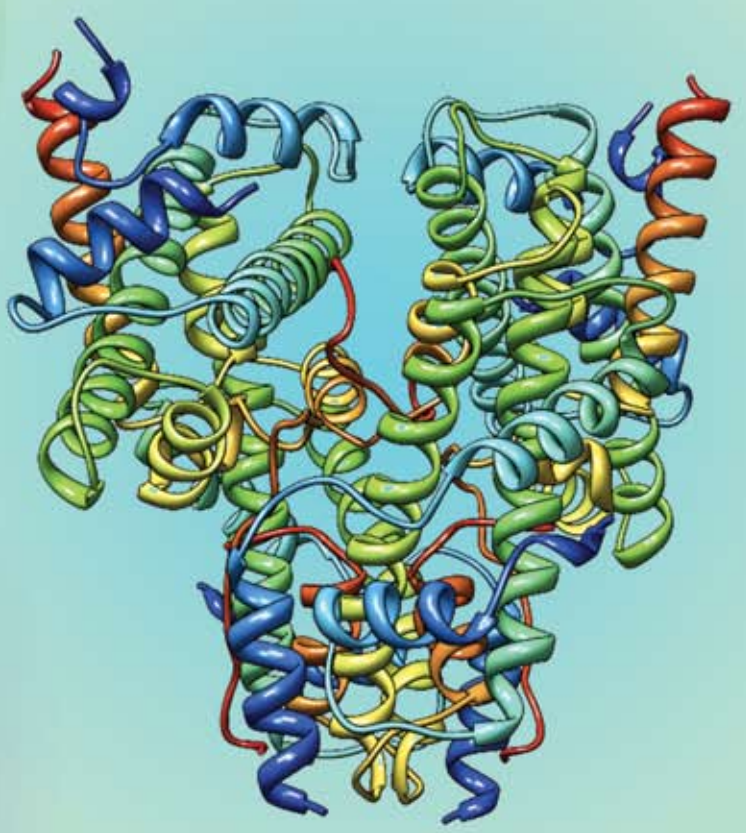
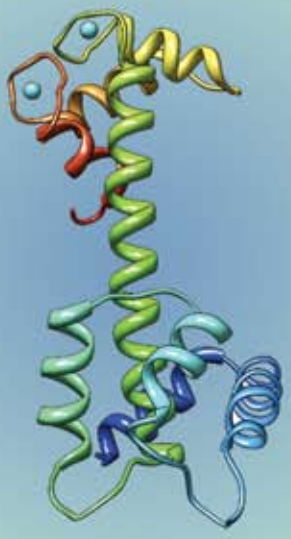
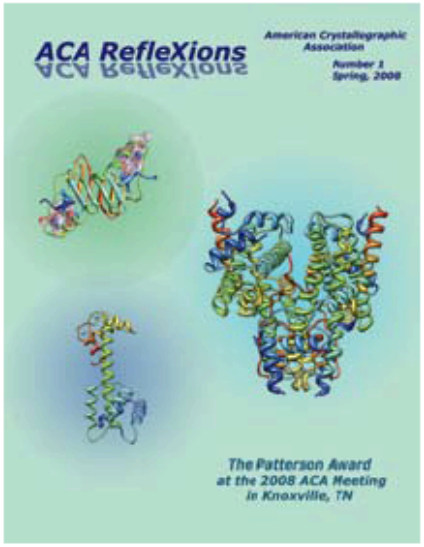






The Patterson Award at the 2008 ACA Meeting in Knoxville, TN



On the Cover:

At the 2008 ACA Meeting in Knoxville the **A. Lindo Patterson Award** will be presented to **Bi-Cheng (B.C.) Wang**, Professor, Dept. of Biochemistry and Molecular Biology and Ramsey/Georgia Research Alliance Eminent Scholar in Structural Biology at the University of Georgia. The images on the cover were selected from many that have special significance to B.C.

At left, top: neurophysin, a hormone carrier protein, in complex with a dipepide. This was the first *de novo* structure solved from SAD data from an incorporated iodine atom using Wang's ISAS solvent flattening program. The asymmetric unit is an elongated tetramer of dimensions 110 x 40 x 30 Å, composed of two dimers related by pseudo twofold symmetry. Each monomer consists of two homologous layers, each with four antiparallel ß-strands. The two regions are connected by a helix followed by a long loop. Monomer-monomer contacts involve antiparallel ß-sheet interactions, which form a dimer with two layers of eight ß-strands. One peptide per monomer occupies the principal hormone-binding pocket formed by part of the amino-terminal region and parts of the connecting helix and loop, with binding to protein consistent with conclusions drawn from solution studies. Dimer-dimer contacts involve the Tyr49 region adjacent to this site. A fifth dipeptide, of unknown biological significance, helps to stabilize one of the monomer-monomer interfaces and the tetramer-tetramer network in the crystal. The image is from *Crystal Structure of a Bovine Neurophysin II Dipeptide Complex at 2.8 Å Determined from the Single-Wavelength Anomalous Scattering Signal of an Incorporated Iodine Atom*, L. Chen, J.P. Rose, E Breslow, D. Yang, W. Chang, W.F. Furey Jr, M. Sax and B.C. Wang, *PNAS USA*, 1991, **88**, 4240-4244. © 1991 by National Academy of Sciences.

At right: **The nucleosomal core (H2A-H2B-H3-H4)$_2$ histone octamer**. This was solved from SIR data using the ISIR solvent flattening program in collaboration with Moudruanakis and colleagues. The histone octamer is a tripartite assembly in which a centrally located (H3-H4)$_2$ tetramer is flanked by two H2A-H2B dimers. It has a complex outer surface; depending on the perspective the structure appears as a wedge or as a flat disk with diameter 65Å and length 60Å at its maximum and ≈ 10Å at the minimum. The histone octamer has regularly spaced ridges and valleys that define a left-handed protein superhelix with ≈28Å pitch, very suggestive of the path of the DNA superhelix in the nucleosome. *The nucleosomal core histone octamer at 3.1 A resolution: A tripartite protein assembly and a left-handed superhelix*, G. Arents, R.W. Burlingame, B.C. Wang, W.E. Love, and E.N. Moudrianakis, *PNAS*, **88**, 10148-10152, (1991).

At left, bottom: troponin C, which was solved from SIR data using B.C.'s ISIR solvent flattening program in collaboration with M. Sundaralingam and colleagues. The structure of troponin C (TnC), the Ca^{2+}-binding subunit of the troponin complex, shows that the protein is about 70 Å long with an unusual dumbbell shape. The carboxyl and amino domains are separated by a single long alpha helix of about nine turns. Only the two high-affinity Ca^{2+}-Mg^{2+} sites of the COOH-domain are occupied by metal ions resulting in conformational differences between the COOH- and NH_2-domains. These differences are probably important in the triggering of muscle contraction by TnC. The structure is relevant in understanding the function of other calcium-regulated proteins, in particular calmodulin because of its strong similarity in amino acid sequence. *Molecular Structure of Troponin C from Chicken Skeletal Muscle at 3Å Resolution*. M. Sundaralingam, R. Bergstrom, G. M. Strasburg, S. T. Rao, P. Roychowdhury, M. L. Greaser and B. C. Wang, *Science* **227**, 945-948 (1985).