M06.BB Structure from Pictures: Direct Macromolecular Structure Determination by Electron Microscopy

Chair: H. Saibil
Co-Chair: R. Henderson

Attendance: 120

This session conveyed some of the progress and excitement of the cryo EM field, with three talks on “single particles” (isolated macromolecular complexes in solution) and two on electron crystallography of two-dimensional (2D) crystals.

The single particle field has been developing rapidly and is a remarkable topic for the IUCr, since it does not involve any crystallography, except in the sense that 3D alignment of randomly oriented complexes is crystallization in the computer. Beginning with rotavirus, BVV Prasad presented a structural analysis of this complex, double-shelled virus caught in the process of transcribing and releasing its RNA through the 5-fold vertices of its icosahedral shell. With a series of low resolution reconstructions of different states of the chaperonin GroEL, Helen Saibil mapped out the domain rotations in the ATPase cycle and interpreted them by docking domain atomic structures into the EM maps. At 10 A resolution, a new inter-ring contact, involved in negative cooperativity, was seen in GroEL-ATP. Bettina Bottcher showed the work that has led to the first complete secondary structure assignment for a protein in a single particle complex. The 7.4 A resolution map of Hepatitis B virus core particles revealed the fold of the alpha-helical capsid protein, recently confirmed by the X-ray crystallographic structure.

Moving to electron crystallography, Vinzenz Unger presented the structure of the gap junction at an in-plane resolution of 7 A, with two apposed hexameric rings forming a channel across two cell membranes. The transmembrane regions were clearly identified as 4-helix segments, and a plausible model was built with a large beta-barrel forming the extracellular seal of the channel. The session ended with the structure determination of the tubulin dimer by electron crystallography, presented by Eva Nogales. The high quality of the image phases meant that the 3.7 A map allowed a complete secondary structure determination, and the localization of bound GTP and taxol. The fold is close to that of the bacterial protein FtsZ, whose structure was determined crystallographically around the same time.

Helen Saibil