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**Advanced Area Detectors for Protein Crystallography and Electron Microscopy.** N.-H. Xuong, Depts. of Physics, Biology, Chemistry & Biochemistry, Univ. of California San Diego, 9500 Gilman Dr, La Jolla, CA 92093-0359 USA.

The search for advanced area detectors for protein crystallography started with the multiwire area detector more than three decades ago. It was soon followed by the development of imaging plate and the charge-coupled device (CCD) based detectors. The working principle and characteristics of these detectors, as well as the latest state-of-the-art, direct solid state detectors, using pixel arrays with application specific integrated circuit (ASIC) read-out, will be discussed. Lately, a new method for solving 3D structures of proteins using cryo-electron microscopy (EM) has emerged. The advantage of cryo-EM over protein crystallography is that it does not require growing large crystals, a very time consuming and, in many cases, impossible task. Cryo-EM, however, has a drawback that it produces only low resolution structures (7Å for a virus, 11Å for a large protein complex). It is estimated that producing a 3Å structure would require a million images and consequently the difficulties connected with the collection and processing of very large data sets is a major hurdle in obtaining higher resolutions. Use of films for recording such large numbers of images is difficult and the standard CCD based detectors do not seem to yield good enough data. A pioneering effort at UCSD to design and build a solid state detector with direct and automatic detection and read-out to overcome the difficulties inherent in using film will be discussed.