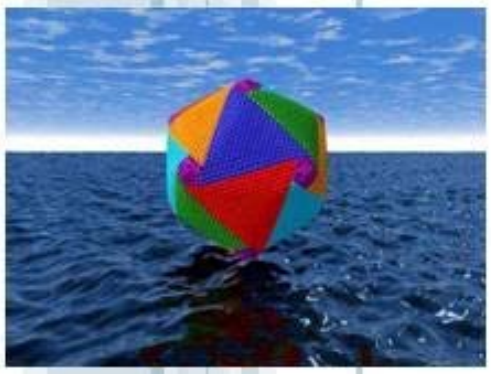
The CUHK Biochemistry Programme

THE MAGIC OF CRYO-EM: FROM TINY TO GIGANTIC



Cryo-electron microscopy (Cryo-EM) is a form of transmission electron microscopy where the samples are observed in their native states at cryogenic temperature. Using computational 3-D reconstruction and combining with X-ray crystallography, Cryo-EM has become an increasingly powerful tool in structural studies of macromolecular assemblies, such as protein complexes and viruses. For instance, many icosahedral viruses have exceptionally high symmetry (at least 60 fold symmetric operations), which greatly facilitates Cryo-EM 3-D reconstruction. As a result, the structures of many icosahedral viruses have been successfully determined by Cryo-EM. Cryo-EM has also been widely used in structural analysis of other low symmetric or even asymmetric macromolecules, such as protein complexes (e.g. GroEL) and ribosomes. Over the past decade, advances in EM technology and computational power have significantly improved the resolution of Cryo-EM: from 2-3 nanometers to sub-nanometer or even atomic level. Thus, accurate structural information of biomacromolecules can be obtained and interpreted at their native states with a resolution close to that of X-ray crystallography. At the other extreme, the size of the samples that can be studied by Cryo-EM has also increased dramatically. Examples include Cryo-EM studies of giant viruses, some of which have diameters close to 1μm. Most recently, cryo-electron tomography (Cryo-ET) technique has made possible to reconstruct 3-D models of cells and extended the boundaries of structural biology.

Speaker: **Professor Chuna Xiao**
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Date: **December 20, 2012 (Thursday)**

Time: **2:30 pm**

Venue: **SC L2, Science Centre,**
The Chinese University of Hong Kong