NANYANG TECHNOLOGICAL UNIVERSITY

School of Biological Sciences

Seminar Announcement

Recent advances in high-resolution cryo-EM structure determination

Date: 19 May 2015 (Tuesday)

Time: 2:30pm to 3:30pm

Venue: SBS-01n-33 Classroom 1

Host: Prof Daniela Rhodes

Speaker: Dr.Bai Xiao-chen
MRC, Laboratory of Molecular Biology,
Cambridge, UK

Abstract

For many years, structure determination of biological macromolecules by cryo-electron microscopy (cryo-EM) was limited to large complexes or low-resolution models. With recent advances in electron detection and image processing, the resolution by cryo-EM is now beginning to rival X-ray crystallography. A new generation of electron detectors record images with unprecedented quality, while new image-processing tools correct for sample movements and classify images according to different structural states. Combined, these advances yield density maps with sufficient detail to deduce the atomic structure for a range of specimens.

Now the question arises as to where the new size limits lie. The ribosome and virus might be considered easy targets for cryo-EM because they are relatively large, and the latter also has high symmetry. Currently, the smallest complex subjected to the new methodology is γ-secretase. This asymmetric membrane complex comprises four different proteins with a total molecular weight of 170 kDa. Imaging on a K2 detector in counting mode and performing reconstruction with a modified motion correction and 3D classification algorithm led to near-atomic resolution, which proved sufficient for *de novo* model building.