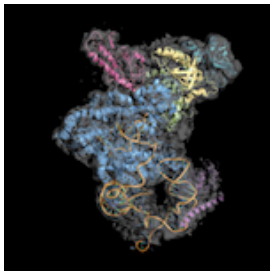

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Short Talk 2 - The CryoEM approach; current and future possibilities

Monday, 19 November 2018 14:15 (20)

In the last years there has been an explosion of the cryo electron microscopy single particle technique to get high-resolution structures of protein complexes. Cryo-EM has grown from a niche technique into one of the major structural biology methods, especially for large macromolecular complexes or membrane proteins hard to crystallise. What has been defined as the “resolution revolution” has been driven by the development of more stable electron optics, more sensitive direct electron detectors and better and faster software for image processing. Major efforts are also devoted to the inventions of new methods for sample preparation and for automation of both cryo-EM data acquisition and image processing. In fact, getting a nice sample for optimal imaging and processing the data to obtain correct and most informative structures, still requires specialists’ skills.
This lecture will run through examples of cryo-EM structures both from the literature and the Swedish cryo-EM facility; it will show the basic steps of image recording and image processing analysis to obtain one or multiple 3D maps. Some examples of cryo electron tomography (cryo-ET) will be also given to illustrate what can be achieved with the cryo-EM microscopes available to Swedish researchers at SciLifeLab

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