Gjønnes Medal Lecture

GM01

From Electron Crystallography to Single Particle CryoEM

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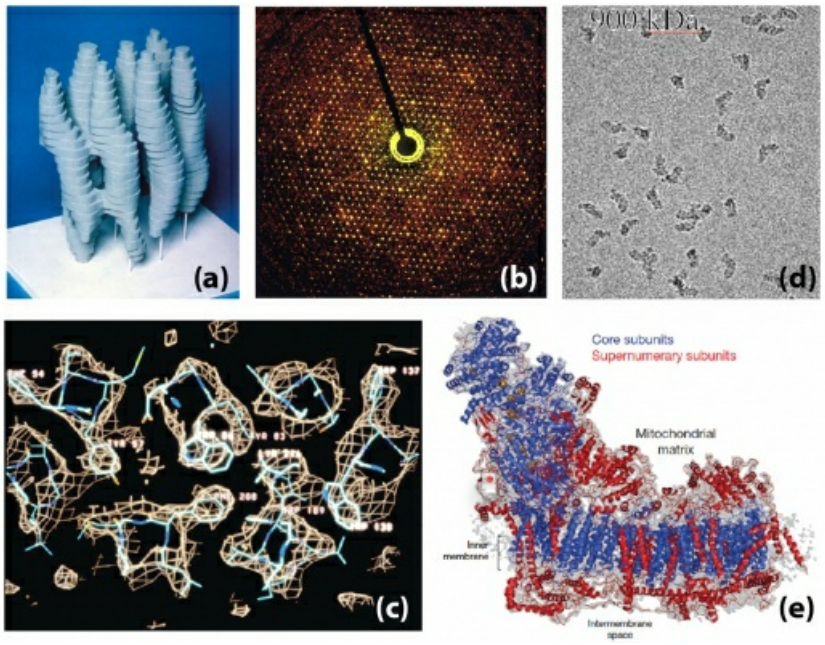
Electron microscopy as a tool for investigating biological structure has increased in power and resolution during recent years. I will describe my own trajectory from X-ray crystallographic analysis of protein structure with 3D crystals to electron crystallographic determination of membrane protein structure in 2D crystals and, most recently, to electron cryo-microscopy (cryoEM) of single particles embedded in thin films of amorphous ice. The panels in the figure show (a) a 3D map of bacteriorhodopsin (bR) from work in collaboration with Nigel Unwin [1]; (b, c) an electron diffraction pattern of 2D crystals of bR, and a section of the 3.5Å map that allowed the first atomic model of bR to be constructed [2]; (d, e) single particle cryoEM images of the 900 kDa mitochondrial Complex I and a 3D model, from a collaboration with Judy Hirst's group in Cambridge [3].

[1] Unwin, P.N.T. & Henderson, R. (1975) J. Mol. Biol. 94, 425-440.
[2] Henderson R. et al (1990) J. Mol. Biol. 213, 899-929.
[3] Vinothkumar, K.R, Zhu, J. & Hirst, J. (2014) Nature 515, 80-84.



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