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## The cryoEM revolution in structural biology

Structural biology has historically been dominated by X-ray crystallography and nuclear magnetic resonance (NMR) spectroscopy, which are incredibly powerful methods. Over 100,000 structures have been determined, with atomic coordinates deposited in the protein data bank (PDB). In the last few years, single particle electron cryomicroscopy (cryoEM), which does not require crystallisation or isotope labelling, has experienced a quantum leap in its capability, due to improved electron microscopes, better detectors and better software, and this is revolutionising structural biology. Using the technique invented by Jacques Dubochet and his colleagues, a thin film containing a suspension of the macromolecules of interest is plunge-frozen into liquid ethane at liquid nitrogen temperature, creating a frozen-hydrated sample in which individual images of the structures can be seen in many different orientations. Subsequent computer-based image analysis is then used to determine the three-dimensional structure, frequently at near-atomic resolution. I will show examples of some recent structures, and discuss remaining barriers to progress. CryoEM is already a very powerful method, but there are still many improvements that can be made before the approach reaches its theoretical limits.

**Monday 20 March 2017 at 4.00 P.M.**

**COFFEE AND TEA WILL BE SERVED AT 3.45 P.M.  
AND DRINKS AT 5.00 P.M. IN FRONT OF THE SOLVAY ROOM**

#### SOLVAY ROOM

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