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The direct electron detector driven revolution in structural biology

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Electron cryo-microscopy, cryoEM, is rapidly replacing X-ray crystallography as the preferred method in structural biology for determining the structures of biological molecules. The rise of cryoEM can be traced to the introduction of higher detective quantum efficiency, DQE, CMOS based direct electron detectors. The resulting improved signal to noise in images of radiation sensitive samples allows near atomic resolution structures to be obtained routinely, with less sample and without the need to first have well diffracting crystals.

CMOS detectors developed for cryoEM differ from the now ubiquitous CMOS optical sensors. The most obvious difference being the need to use enclosed geometries to limit the radiation damage associated with detecting electrons. Optimisation for DQE in electron detection also requires sensors to be backthinned and operated in a counting mode. In the counting mode a final image is assembled from processed images of the individual incident electrons. To be practical this requires both fast frame rate and image processing.

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