

High-resolution cryo-electron microscopy: advances and challenges in image analysis

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Improvements in detector technology and computational imaging have transformed cryo-Electron Microscopy (EM) into a powerful strategy for structure determination that can be used to study a broad spectrum of biomedical targets. The resolutions achieved in some cases are high enough to reveal atomic level protein-compound interactions that are relevant for drug discovery. In particular, the ability to sort out structural heterogeneity combined with the capability of direct electron detectors to operate in movie mode, has provided unique opportunities for the development of effective algorithmic strategies capable of teasing out high-resolution information from noisy microscopy images. I will give an overview of recent developments in the field that have enabled the routine structural characterization of challenging targets at unprecedented levels of detail, and will also highlight some of the remaining challenges in computational image analysis that would need to be addressed in order to further advance the frontiers of cryo-EM.