

Grid preparation and data Collection for cryo-EM

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Cryo-EM has transformed structural biology and many other biological research areas due to recent technical advances including improved electron detectors and image-processing algorithms. Compared to X-ray crystallography, cryo-EM allows structural determination of large and heterogenous macromolecular complexes in their native state with very little sample. It is now possible, in some ideal cases, to determine a protein structure by single-particle cryo-EM from data collected in a few hours. Despite the advances, many challenges remain for routinely obtaining high-resolution structures. One of the challenges is grid preparation, which is usually decisive for successful data collection and structure determination. In my lectures, I will discuss how to design experiments for freezing cryo-EM grids and strategies for data collection.