

W0020

Electron Cryomicroscopy of Macromolecular Assembly at Subnanometer Resolution. W. Chiu, National Center for Macromolecular Imaging, Baylor College of Medicine, Houston, TX 77030.

Electron cryomicroscopy has been advanced to resolve structures of large macromolecular assemblies at resolution range of 5-10 Å without using crystals. At this resolution, we are able to resolve long alpha helices and large beta sheets of protein components or subunit domains of the assembly. Using model building, the folds of components and domains may be derived. Alternatively, if the crystal structures of components and domains are known, they can be docked into the cryomicroscopy density map by rigid body or flexible fitting. A valuable application of electron cryomicroscopy is to study the structural changes of assembly during different physiological states. Currently, all these structural informatics are not easily accessible to the public. An extension of the already successful infrastructure of PDB to archive the electron cryomicroscopy density map is certainly timely and critical. Such a publicly accessible structural informatics will provide biological end-users to mine structures and other biological information to understand structure and function relationship of assemblies which are the building blocks of physiological processes.

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