Three-dimensional electron microscopy of macromolecular assemblies

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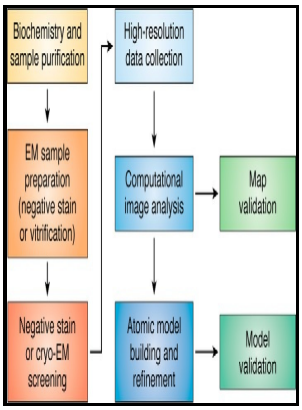

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Notes: Includes bibliographical references (p. 293-331) and index.
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This tool has several advantages over the conventional structural biology tools X-ray crystallography and NMR such as, structure elucidation without crystallization, solving the structure in physiological conditions, and with literally no upper limit on size of the protein. Negative staining can reveal the true solvent-excluded surface and shape of a biological molecule. De Carlo S, Harris JR.

Electron Microscopy of Macromolecular Assemblies

Rossmann MG, Bernal R, Pletnev SV. MODELLER, which is a homology modelling tool commonly used with X-ray and NMR structures as templates, also incorporates two fitting modules — Mod-EM for rigid fitting Topf et al. Visualizing density maps with UCSF Chimera.

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Specimen preparation methods for electron microscopy The most commonly used staining methods in electron microscopy are negative staining, CryoEM and Cryo-negative staining. Recent studies on Limulus SAP-like pentraxin Shrive et al. The poor contrast that is inherent in the cryoEM sets a lower limit of about 200 kDa on the protein size.

Three dimensional electron microscopy and in silico tools for macromolecular structure determination.

Similarly, one can also use the SITUS package for fitting crystal structures by both rigid body and flexible way Wriggers et al. Cryo-negative staining Cryo-negative staining combines the advantages of both negative staining and cryo-EM. This approach is known to give higher resolution structural details but suffers from poor contrast and high radiation damage.

Three

Talmon Y, Davis HT, Scriven LE, Thomas EL. Annu Rev Biophys Biomol Stuct 2002;31: 303-19.

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