

## Interplay between EM and X-ray: Molecular replacement and electron density averaging

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As structural biology is now focusing more on multi-component molecular complexes, the interplay between X-ray crystallography and electron microscopy (EM) has increased. The low-resolution EM image can be used for X-ray structure determination by molecular replacement (MR) and subsequent phase extension to higher resolution by density modification techniques, such as electron density averaging. Case studies will be presented for using EM maps as models for crystal structure solution by various molecular replacement programs such as AMoRe, MolRep and Phaser. Techniques for manipulating the EM image, effects of EM magnification error on structure solution, and effects of positional/rotational errors in the MR solution on phase extension will be discussed. A general use of electron density averaging, between common (or even homologous) sub-regions of any crystals, and between X-crystallography and EM, will be demonstrated.