

## Microsymposium

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### *Cryo-EM in the age of X-ray crystallography*

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Recent breakthroughs in cryo-EM have enabled the determination of biological structures which have previously eluded crystallography. This presentation will discuss the fundamental differences of this modality and introduce the advantages and challenges of the single particle averaging workflow. Since the common denominator between both techniques is the reciprocal space dataset, it is possible to phase x-ray datasets with low resolution cryo-EM envelopes as well as apply established crystallographic methods for model coordinate refinement to cryo-EM maps. The future will certainly see a tighter integration of both modalities and more user friendly software for image collection and processing of cryo-EM data.

**Keywords:** [Cryo electron microscopy](#)