

## Challenges for high-resolution 3D cryo-EM of macromolecular complexes: a case study of RNA Pol III and TMV

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The emergence of direct electron detectors and improvements in image processing algorithms has led to a resolution leap for cryo-EM reconstructions of macromolecular complexes, often approaching near-atomic resolution and allowing for the building of atomic models de novo. Obtaining accurate structural information from EM density maps depends on suitable image acquisition schemes that minimise radiation damage to preserve high-resolution features, as well as tools for the refinement and validation of the resulting atomic models that are tailored towards the specific challenges of data from cryo-EM. I will discuss some of these developments based on our experience with RNA polymerase III and TMV.