

## **CryoEM Reveals Unpredictable Structural Details of Protein and RNA**

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Cryogenic electron microscopy (cryoEM) has been advanced to resolve atomic structures of biochemically purified macromolecules with details equivalent to X-ray crystal structures. A unique aspect of cryoEM is to use image processing methods to sort out images of particles with heterogeneous compositions and conformations. This allows us to visualize structures of macromolecules that exist in an ensemble of biochemical states, which are interpretable in their biochemical processes. I will illustrate this approach to show how different folding intermediates of tubulin is seen within the chamber of human chaperonin TRiC and how misfolded and folded states of ribozyme are organized.