

# Cryo-electron Microscopy Resolution Revolution Viewed Through the Lens of the Protein Data Bank

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Cryo-electron microscopy (cryo-EM) has evolved rapidly over the past decade into a mainstream tool for structural biologists. The pace of technical development and innovation in this field has been striking, going from 'blobology' views of negatively-stained samples to high-resolution, three-dimensional (3D), atomic-level structures of diverse cryogenically cooled biological macromolecules and their complexes with one another and with small-molecule ligands. The success of cryo-EM is evident from the flood of 3D electron microscopy (3DEM) structure data pouring into the Protein Data Bank and the Electron Microscopy Data Bank (EMDB). Both of these digital data resources are Worldwide Protein Data Bank (wwPDB, [wwpdb.org](http://wwpdb.org)) Core Archives, jointly managed by the wwPDB partnership (RCSB Protein Data Bank, Protein Data Bank in Europe, Protein Data Bank Japan, Electron Microscopy Data Bank, and Biological Magnetic Resonance Bank). In the public domain today, there are nearly 20,000 3DEM experimental maps (stored in EMDB) and ~11,000 atomic-level 3DEM structures (stored in PDB), all freely available with no limitations on usage. This presentation will provide an overview of 3DEM holdings in the PDB and wwPDB validation methods used to assess the quality of 3DEM structures, with particular emphasis on analysis tools and visualization features provided at no charge to data consumers on the RCSB Protein Data Bank research-focused web portal (RCSB.org).