

## Perspectives on the cryo-EM “Resolution Revolution” from the Protein Data Bank

Stephen K. Burley, Director  
RCSB Protein Data Bank  
Institute for Quantitative Biomedicine  
Rutgers, The State University of New Jersey  
174 Frelinghuysen Road  
Piscataway, NJ 08854

Recent technical advances in electron microscope design, automated cryogenic sample handling, direct electron detection, phase plate optics, and data processing software have ushered in an exciting new era in electron microscopic studies of biological systems. Under favorable circumstances, single-particle methods are yielding near atomic resolution ( $\sim 2\text{\AA}$ ) structures of large macromolecular assemblies. Equally exciting are the insights coming from cryo-electron tomography using sub-tomogram averaging and micro-electron diffraction. The impact of these related methodologies and structures therefrom will be discussed from the perspective of the RCSB Protein Data Bank (RCSB PDB; [rcsb.org](http://rcsb.org)).

**Acknowledgements:** The RCSB PDB is a member of the Worldwide Protein Data Bank organization ([wwPDB; wwpdb.org](http://wwPDB.org)), which manages the Protein Data Bank archive. Core RCSB PDB operations are funded by a grant to SKB (NSF DBI-1338415) from the National Science Foundation, the National Institutes of Health, and the US Department of Energy.