

# New electron microscopy database and deposition system

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Electron cryomicroscopy (cryo-EM) has established itself as a powerful tool for the study of the structure and function of biological macromolecules. Resolutions of ~4–5 Å for single particles and ~3 Å for 2D-crystals are now possible through recent improvements in technology and data processing associated with this cryo method.

These improvements to the resolution of structures solved by EM have arisen through increased preservation and maintenance of native structure by immobilizing the specimen in a thin layer of vitrified buffer by rapid freezing. Recent improvements in electron microscope technology (high-coherence electron sources, increased accelerating voltages) and in data processing (faster processing, better algorithms for particle classification, alignment and reconstruction) have also made differences.

The number of macromolecular complexes of biological relevance that await structural characterization is still very large, and for many of these cases, such complexes are not available in sufficient quantities for crystallization trials or are too unstable or flexible to form crystals at all. Therefore their structures cannot be readily determined by X-ray crystallography techniques. As a consequence, biologists worldwide are now using cryo-EM equipment to analyse these multitudes of complexes.

In order to manage, organize and disseminate the data on the structure of macromolecules solved by 3D electron

The screenshot displays the 'EM-Deposition Tool For Electron Microscopy Volume Data' interface. On the left, there is a navigation menu for 'IIMS submission-1022' with options like 'Contact Information', 'Instruction to EMDB', 'File Description', 'Title, Author and Reference', 'Sample Details', 'Sample Components', 'Experimental Details', 'Vitrification', 'Imaging', 'Image Processing', '3D-Reconstruction', '3D-Fitting', and 'Misc'. The main area is titled 'Sample Details' and contains a form with the following fields: 'Enter name of sample', 'Select aggregation state', 'Enter the oligomeric state of the sample', 'Enter the number of unique components in the Sample', 'Enter the experimental molecular weight of the sample', 'Enter theoretical molecular weight of sample', 'Enter method of determination of molecular weight of sample', and 'Enter any additional sample details'. A 3D molecular model of a protein complex is shown on the right side of the form.

microscopy, an electron microscopy database has been set up at the European Bioinformatics Institute (<http://www.ebi.ac.uk/msd-srv/emdep/>). The New 3D-EM database provides a facility for storing volume maps, relevant textual descriptors and data files containing figures and sections. Where applicable, the database also contains layer-line data and structure factor files. The deposition system has been active since June 2002.

The expected further development of cryo-EM techniques and of single-particle image processing methods, together with higher throughput from increased automation and higher resolution, will continue to expand the number of

structures solved and hence the requirement for a secure archive.

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