



Seminar/Talk

Cryo-electron tomography: The power of seeing the whole picture

Wolfgang Baumeister

Max Planck Institute of Biochemistry

Host: Peter Jonas

Cryo-electron tomography: The power of seeing the whole picture Traditionally, structural biologists have approached cellular complexity in a reductionist manner by studying isolated and purified molecular components. This 'divide and conquer' approach has been highly successful, as evidenced by the impressive number of entries in the PDB. However, awareness has grown in recent years that only rarely biological functions can be attributed to individual macromolecules. Most cellular functions arise from their acting in concert. Hence there is a need for methods developments enabling studies performed in situ, i.e. in unperturbed cellular environments. Sensu stricto the term 'structural biology in situ' should apply only to a scenario in which the cellular environment is preserved in its entirety. Cryo electron tomography (Cryo ET) has unique potential to study the supramolecular architecture or 'molecular sociology' of cells. It combines the power of three-dimensional imaging with the best structural preservation that is physically possible to achieve. We have used cryo-electron tomography to study the 26S proteasome, the main machinery for protein degradation, in a number of cellular settings revealing its precise location, assembly and activity status as well as its interactions with other molecular players of the cellular protein quality control machinery. Another pathway for the disposal of waste is autophagy. Cryo ET has allowed to visualize the biogenesis of autophagosomes in great detail. For realizing the full potential of cryo ET, further advances in technology and methodology are needed. Baumeister W.: Cryo-electron tomography: A long journey to the inner space of cells, *Cell*, 185(15):2649-2652 (2022)

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Central Bldg / O1 / Mondl 2 (I01.O1.008)



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