

Protein structure determination using cryo-EM and tomography

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Cryo-EM is a very powerful tool to determine the structure of proteins and protein complexes. Improvements in the hardware for data collection and the software used for data processing has led to a steep increase in the number of structures solved by cryo-EM. Here I will present two examples of how cryo-EM can be used to solve structures of proteins, focusing on proteins involved in secretion. I will show how single-particle cryo-EM was used to obtain the sub-nanometer resolution structure of a 190KDa enzyme involved in bacterial secretion. I will then move on to a more complex eukaryotic system, where secretion is mediated by protein coats assembled on membranes and I will show how cryo-tomography and sub-tomogram averaging can be used to solve the architecture of the coat on membranes.